

## SUPPLEMENTAL FIGURE LEGENDS

**Supplemental Figure S1.** ChIP Analysis for the GL2 Binding to the *LRL1* and *LRL3* Upstream Regions.

**(A)** The regions amplified in the ChIP analysis, *LRL1*-S1, *LRL1*-N, *LRL1*-S2 and *LRL3*-N, are schematically illustrated. The L1 box-like sequence exists in *LRL1*-S1 and *LRL1*-S2, but not in *LRL1*-N or *LRL3*-N.

**(B)** Results of the ChIP analysis of the regions illustrated in **(A)** are shown. Relative enrichment folds (anti-GFP/IgG) in *GL2pro-GFP-GL2/gl2-5* roots and wild-type roots are shown in white and gray boxes, respectively (mean  $\pm$  s.d.,  $n = 3$ ). Asterisks indicate significant differences between the enrichment folds in *GL2-pro-GFP-GL2/gl2-5* and in the wild type (\*  $P < 0.05$ ; \*\*  $P < 0.01$ , Student's *t*-test).

**Supplemental Figure S2.** Expression Analysis of the *lrl1-2* and *lrl2-2* Mutant Genes.

**(A)** The gene structures and T-DNA insertion sites of *lrl1-2* (SALK\_006430) and *lrl2-2* (SALK\_029317c) are schematically illustrated. Horizontal arrows labeled with F and R indicate the locations of the PCR primers used in **(B)**.

**(B)** The results of semi-quantitative RT-PCR analysis for *LRL1* and *LRL2* transcripts in wild-type and mutant plants are shown. Transcripts of the *TUBULIN2* (*TUB2*) gene were used as reference.

**Supplemental Figure S3.** Expression Patterns and Intensities of bHLH-GFP Fusion Proteins Driven by the *GL2* Promoter.

The GFP fluorescence signals in transgenic roots harboring *GL2pro-RHD6-GFP* **(A)**, *GL2pro-RSL1-GFP* **(B)**, *GL2pro-RSL2-GFP* **(C)**, *GL2pro-LRL1-GFP* **(D)**, and

*GL2pro-LRL2-GFP* (E) are shown. Bar = 100  $\mu$ m

**Supplemental Figure S4.** Root Hair Development Patterns of the Transgenic Plants Harboring the *GL2* Promoter-driven bHLH-GFP Genes.

PI-stained epidermal cells of wild-type (A) and *gl2-5* (B) roots, and transgenic roots harboring *GL2pro-RHD6-GFP* (C), *GL2pro-RSL1-GFP* (D), *GL2pro-RSL2-GFP* (E), *GL2pro-LRL1-GFP* (F), *GL2pro-LRL2-GFP* (G), *GL2pro-VP16-GL2 $\Delta$ N* (H), and *GL2pro-LRL1-GFP* and *GL2pro-RHD6-GFP* (I) are shown. N and H cell files, the identities of which were judged by the fact that cells in N cell files are longer than those in H cell files, are marked by “N” and “H”, respectively. Arrowheads and Arrows indicate ectopic root hairs developing from N cell files and branching root hairs, respectively. Bar = 25  $\mu$ m

**Supplemental Figure S5.** Trichome Phenotypes of Transgenic Plants Harboring Both *GL2pro-LRL1-GFP* and *GL2pro-RHD6-GFP*.

Trichomes of wild-type plants (A) and transgenic plants harboring both *GL2pro-LRL1-GFP* and *GL2pro-RHD6-GFP* (B to D) are shown. Bar = 250  $\mu$ m

**Supplemental Figure S6.** Sequences Surrounding the L1 Box-like Sites Recognized by GL2.

DNA sequences surrounding the L1 box-like sites that have confirmed to be bound to GL2 individually by ChIP analysis are aligned. The sites *CESA5-S*, *MYB23-S*, *PAP2-S*, and *MYB113-S* correspond to the L1 box-like sites 802-, 2,372-, 1755-, and 837-base upstream from their initiation codons, respectively. The other sites are the same as those shown in Table II. The sites, *RSL2-S3-1*, *RSL2-S3-2*, *LRL1-S1-1*,

*LRL1-S1-2*, and those in the *TT8* promoter region are omitted because they were examined for GL2 binding to more than one copy of the L1 box like-sequence. The L1 box-like sequence is highlighted. Frequently appearing bases (at 50% or higher) at each position are shadowed. The sequence composed of the frequently appearing bases is shown below the alignment.

864 genes the steady-state transcript levels of which were consistently up-regulated by the dexamethasone (DEX) treatment of the 35pro-VPI6GLZLN seedlings more than 2-fold in triplicated microarray experiments are listed.

Gene ID	average fold-change	DEX-A vs DMSO-A Signal fold-change	DEX-A vs DMSO-A Change p-value	DEX-B vs DMSO-B Signal fold-change	DEX-B vs DMSO-B Change p-value	DEX-C vs DMSO-C Signal fold-change	DEX-C vs DMSO-C Change p-value	DEX-D vs DMSO-D Signal fold-change	DEX-D vs DMSO-D Change p-value	Annotation
260124.at	977.76	382.04	0.00002	2194.99	0.00002	1176.27	0.00002	1176.27	0.00002	UBC31 (UBQUITIN-CONJUGATING ENZYME 31); ubiquitin-protein ligase
260223.at	291.88	109.50	0.00002	784.99	0.00002	207.94	0.00002	207.94	0.00002	pectinesterase family protein
260561.at	176.88	388.02	0.00002	92.51	0.00002	197.59	0.00002	197.59	0.00002	chitinase, putative
260166.at	116.70	97.01	0.00002	1371.18	0.00002	119.43	0.00002	119.43	0.00002	GL3 (GLABRA 2); DNA binding / transcription factor
260618.at	111.43	194.01	0.00002	64.00	0.00002	111.43	0.00002	111.43	0.00002	H04 (HEME OXYGENASE 4); heme oxygenase (decyclizing)/ oxidoreductase
265672.at	103.97	103.97	0.00002	32.00	0.00002	222.86	0.00002	222.86	0.00002	cysteine proteinase inhibitor-related
260770.at	103.97	59.71	0.00002	27.86	0.00002	315.17	0.00002	315.17	0.00002	glycosyl hydrolase family 17 protein
264423.at	51.98	55.72	0.00002	39.40	0.00002	64.00	0.00002	64.00	0.00002	BGLU45; hydrolase, hydrolyzing O-glycosyl compounds
257163.at	43.21	59.71	0.00002	45.25	0.00002	45.25	0.00002	45.25	0.00002	MYB3051 (myb domain protein 305); DNA binding / transcription factor
262711.at	43.21	42.22	0.00002	42.22	0.00002	45.25	0.00002	45.25	0.00002	similar to unknown protein [Arabidopsis thaliana] (TAIRAT1G37160.1); similar to unnamed protein product [Vitis vinifera] (GB:CA047911.1)
252227.at	42.22	42.22	0.00002	18.38	0.00002	97.01	0.00002	97.01	0.00002	BTB/POZ domain-containing protein
251673.at	40.32	55.72	0.00002	16.00	0.00002	73.52	0.00002	73.52	0.00002	BG3 (BETA-1,3-L-GALACTANASE 3); hydrolase, hydrolyzing O-glycosyl compounds
252959.at	38.40	38.76	0.00002	21.11	0.00002	78.79	0.00002	78.79	0.00002	proton-dependent oligopeptide transport (POT) family protein
259874.at	38.40	48.50	0.00002	18.38	0.00002	68.59	0.00002	68.59	0.00002	esterase/lipase/thioesterase family protein
245159.at	32.75	34.30	0.00002	34.30	0.00002	29.86	0.00002	29.86	0.00002	RALFL18 (RALF-LIKE 18)
247205.at	32.75	90.51	0.00002	8.57	0.00002	45.25	0.00002	45.25	0.00002	PROPEP2 (Elicitor peptide 2 precursor)
252555.at	32.00	55.72	0.00006	13.00	0.00023	45.25	0.00008	45.25	0.00008	alpha-xylotriase, putative
268912.at	32.00	39.40	0.00002	12.13	0.00002	68.59	0.00002	68.59	0.00002	similar to unknown protein [Arabidopsis thaliana] (TAIRAT3G01380.1); similar to l. related (Medicago truncatula) (GB:ABD32828.1); contains domain P
249940.at	30.55	59.71	0.00002	48.50	0.00023	9.85	0.00002	9.85	0.00002	ANAC090 (ARABIDOPSIS NAC domain containing protein 90); transcription factor
259574.at	29.86	42.22	0.00002	13.93	0.00002	45.25	0.00002	45.25	0.00002	MLP168 (MLP-LIKE PROTEIN 168)
259953.at	29.86	29.86	0.00002	27.86	0.00002	32.00	0.00002	32.00	0.00002	BDR5; anion exchanger
245710.at	28.51	38.76	0.00002	14.93	0.00002	42.22	0.00002	42.22	0.00002	carbonic dehydratase, putative / carbonate dehydratase, putative
267287.at	27.86	42.22	0.00002	17.15	0.00002	32.00	0.00002	32.00	0.00002	CYP11B9 (cytochrome P450, family 71, subfamily B, polypeptide 9); oxygen binding
249117.at	27.86	24.25	0.001336	29.86	0.000035	29.86	0.000046	29.86	0.000046	AT-HSFABA (Arabidopsis thaliana heat shock transcription factor ABA); DNA binding / transcription factor
264912.at	27.22	39.40	0.00003	14.93	0.000027	34.30	0.00003	34.30	0.00003	psuedogene, aldo/keto reductase family, contains Pfam profile PF00248; oxidoreductase, aldo/keto reductase family, blastp match of 71% identity and unknown protein
266394.at	27.22	34.30	0.000027	13.93	0.00002	42.22	0.00002	42.22	0.00002	unknown protein
249277.at	25.99	103.97	0.00002	13.93	0.00002	12.13	0.00002	12.13	0.00002	GDSL-motif lipase/hydrolase family protein
249491.at	25.99	39.40	0.000428	14.93	0.000214	22.86	0.00002	22.86	0.00002	germin-like protein, putative
249757.at	25.99	21.11	0.00004	38.76	0.00002	22.86	0.00002	22.86	0.00002	proline-rich family protein
260086.at	25.40	78.79	0.00002	9.19	0.000023	22.86	0.00002	22.86	0.00002	GDSL-motif lipase/hydrolase family protein
264082.at	24.25	24.25	0.00002	19.70	0.00002	29.86	0.00002	29.86	0.00002	unknown protein
259735.at	23.70	25.99	0.00002	17.15	0.00002	29.86	0.00002	29.86	0.00002	unknown protein
253459.at	22.63	73.52	0.00002	14.93	0.00002	10.56	0.00002	10.56	0.00002	unknown protein
253782.at	22.11	21.11	0.00002	24.25	0.00002	24.25	0.00002	24.25	0.00002	dihydrooxonotriose aldolase, putative
247213.at	22.11	27.86	0.00002	14.93	0.00002	25.99	0.00002	25.99	0.00002	ATPEP1/PROPEP1 (Elicitor peptide 1 precursor)
250702.at	21.61	19.70	0.00002	12.13	0.00002	42.22	0.00002	42.22	0.00002	peroxidase, putative
255924.at	21.11	22.63	0.00002	22.63	0.00002	18.38	0.00002	18.38	0.00002	phosphoglycerate/bisphosphoglycerate mutase family protein
261737.at	21.11	21.11	0.000035	13.93	0.000214	32.00	0.000552	32.00	0.000552	leucine-rich repeat family protein
259556.at	20.16	17.15	0.00002	19.70	0.00002	24.25	0.00002	24.25	0.00002	hydrolase, alpha/beta fold family protein
261965.at	20.16	18.38	0.00002	14.93	0.00002	14.93	0.00002	14.93	0.00002	ATMKK7 (MAP KINASE KINASE 7); kinase
264638.at	19.70	29.86	0.00002	13.93	0.00002	18.38	0.00002	18.38	0.00002	FL FLOWERING LOCUS T
262843.at	19.25	9.85	0.00002	51.98	0.00002	13.93	0.000552	13.93	0.000552	ATHB32 (ARABIDOPSIS THALIANA HOMEBOX PROTEIN 32); DNA binding / transcription factor
250344.at	18.81	24.25	0.00002	14.93	0.00002	19.70	0.00002	19.70	0.00002	glutaredoxin family protein
263841.at	18.81	19.70	0.00002	17.15	0.00002	19.70	0.00002	19.70	0.00002	xyloglucan/xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative
263944.at	18.81	34.30	0.00006	8.00	0.00002	24.25	0.000167	24.25	0.000167	transposable element, gene
250776.at	17.55	13.93	0.00002	16.00	0.00002	16.00	0.00002	16.00	0.00002	monooxygenase, putative (MO3)
251627.at	17.55	9.85	0.00002	17.15	0.00002	32.00	0.00002	32.00	0.00002	BG1 (BETA-1,3-L-GALACTANASE 1); hydrolase, hydrolyzing O-glycosyl compounds
247447.at	17.15	13.00	0.000114	4.00	0.000078	97.01	0.00002	97.01	0.00002	proton-dependent oligopeptide transport (POT) family protein
247448.at	17.15	16.00	0.00002	16.00	0.00002	19.70	0.00002	19.70	0.00002	similar to unknown protein [Arabidopsis thaliana] (TAIRAT3G27880.1); similar to unknown protein [Vitis vinifera] (GB:CAN65788.1); contains InterF
250734.at	17.15	16.00	0.00002	17.15	0.00002	18.38	0.00002	18.38	0.00002	similar to unknown protein [Arabidopsis thaliana] (TAIRAT3G1600.1); similar to unnamed protein product [Vitis vinifera] (GB:CA015841.1)
252388.at	17.15	13.00	0.00002	13.00	0.000027	29.86	0.00002	29.86	0.00002	CYP94B3 (cytochrome P450, family 94, subfamily B, polypeptide 3); oxygen binding
264900.at	17.15	24.25	0.00002	6.00	0.00002	25.99	0.00002	25.99	0.00002	GP72 (glucose-6-phosphate phosphatase translocator 2; antiporter / glucose-6-phosphate transmembrane transporter
249965.at	16.78	19.70	0.00002	13.93	0.00002	12.13	0.00002	12.13	0.00002	similar to unknown protein [Arabidopsis thaliana] (TAIRAT3G2340.1); similar to unknown protein [Arabidopsis thaliana] (TAIRAT3G2340.1); similar to
258306.at	16.00	14.93	0.000114	4.59	0.000023	59.71	0.00002	59.71	0.00002	ATZIP42 (ARABIDOPSIS THALIANA BASIC LEUCINE-ZIPPER); DNA binding / protein heterodimerization / protein homodimerization / transcription
256602.at	15.63	48.50	0.00003	4.00	0.00006	4.00	0.000046	4.00	0.000046	similar to AT14A [Arabidopsis thaliana] (TAIRAT3G28290.1); similar to AT14A [Arabidopsis thaliana] (TAIRAT3G28290.1); contains InterPro domain P
257082.at	15.63	19.70	0.00002	34.30	0.000078	5.66	0.000389	5.66	0.000389	COBL10 (COBRA-LIKE PROTEIN 10 PRECURSOR)
266392.at	15.28	39.40	0.000147	4.92	0.000225	18.38	0.000037	18.38	0.000037	M10
255364.at	14.83	6.96	0.00002	6.96	0.00002	18.38	0.00002	18.38	0.00002	WRKY87 (WRKY DNA-binding protein 87); transcription factor
248807.at	14.59	21.11	0.00002	14.93	0.00002	9.85	0.00002	9.85	0.00002	pectinesterase family protein
260046.at	14.59	16.00	0.00002	9.19	0.00002	21.11	0.00002	21.11	0.00002	calmodulin binding
245194.at	14.25	17.15	0.00002	12.13	0.00002	13.93	0.00002	13.93	0.00002	protein phosphatase 2C, putative / PP2C, putative
248545.at	14.25	17.15	0.00002	8.57	0.000023	19.70	0.00002	19.70	0.00002	cysteine proteinase, putative
250583.at	13.93	38.76	0.00002	6.96	0.00002	10.56	0.00002	10.56	0.00002	PE1; nucleic acid binding / transcription factor
264632.at	13.83	88.59	0.00013	6.96	0.000068	6.96	0.00002	6.96	0.00002	lecithin:cholesterol acyltransferase family protein / LACT family protein
264566.at	13.83	11.31	0.00002	13.93	0.00002	13.93	0.00002	13.93	0.00002	similar to unknown protein [Arabidopsis thaliana] (TAIRAT3G2310.1)
257766.at	13.61	21.11	0.00002	12.13	0.00002	9.85	0.00002	9.85	0.00002	similar to unknown protein [Arabidopsis thaliana] (TAIRAT3G1000.2); similar to transcription factor [Arabidopsis thaliana] (TAIRAT3G1000.1); similar
258746.at	13.61	64.00	0.00002	5.66	0.00002	6.96	0.000035	6.96	0.000035	germin-like protein, putative
264130.at	13.61	13.00	0.00002	12.13	0.00002	16.00	0.00002	16.00	0.00002	similar to unknown protein [Arabidopsis thaliana] (TAIRAT1G18500.1); similar to unnamed protein product [Vitis vinifera] (GB:CA047911.1)
245276.at	13.30	13.00	0.00002	9.85	0.00002	18.38	0.00002	18.38	0.00002	ATHB-2 (ARABIDOPSIS THALIANA HOMEBOX PROTEIN 2); DNA binding / transcription factor
246144.at	13.30	12.13	0.00002	10.56	0.00002	13.93	0.00002	13.93	0.00002	yeast light chain, putative
254425.at	13.30	5.66	0.00002	5.66	0.00003	13.93	0.00002	13.93	0.00002	similar to unknown protein [Arabidopsis thaliana] (TAIRAT4G05018.1); similar to unnamed protein product [Vitis vinifera] (GB:CA018665.1)
264655.at	13.00	5.66	0.00002	13.93	0.00002	13.00	0.00002	13.00	0.00002	fringe-related protein
261712.at	13.00	18.38	0.00002	9.85	0.00002	12.13	0.00002	12.13	0.00002	alcohol dehydrogenase, putative
249004.at	12.70	4.59	0.000189	12.13	0.000818	38.76	0.00002	38.76	0.00002	unknown protein
254773.at	12.70	27.86	0.00002	6.00	0.000046	12.13	0.00002	12.13	0.00002	ATCSLA15 (Cellulose synthase-like A15); transferase, transferring glycosyl groups
266321.at	12.70	13.93	0.00002	11.31	0.00002	13.00	0.00002	13.00	0.00002	CYP7B48 (cytochrome P450, family 78, subfamily A, polypeptide 8); oxygen binding
254585.at	12.41	13.00	0.00002	12.13	0.00002	12.13	0.00002	12.13	0.00002	AT1BYB6 (BZIP/WRKY-LIKE 6); DNA binding / protein binding / transcription factor / transcription regulator
248247.at	12.41	7.46	0.00002	14.93	0.000023	17.15	0.000023	17.15	0.000023	SPECH (SPEECHLESS); DNA binding / transcription factor
252143.at	12.13	16.00	0.00002	12.13	0.00002	9.19	0.00002	9.19	0.00002	kinasin motor family protein
250968.at	11.85									

255577.at	AT4G01410	729	6.50	0.00002	8.00	0.00002	7.46	0.000027	harpin-induced family protein / HBN1 family protein / harpin-responsive family protein
261846.at	AT1G11540	729	6.96	0.00002	6.96	0.00002	8.00	0.000002	similar to unknown protein [Arabidopsis thaliana] (TAIRAT1G11540.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO38814.1); contains
264129.at	AT1G09170	729	3.48	0.00167	4.00	0.00023	27.86	0.000008	unknown protein
267591.at	AT2G28705	729	5.66	0.00002	6.96	0.00002	7.46	0.000002	DVL1/RTFL8 (ROTUNDIFOLIA LIKE 8)
245886.at	AT5G11020	713	7.46	0.00002	6.50	0.00002	7.46	0.000002	kinase
246989.at	AT5G67350	713	4.59	0.00002	8.00	0.00002	9.85	0.000002	unknown protein
251370.at	AT3G06450	713	7.46	0.00002	6.06	0.00002	8.00	0.000002	similar to unknown protein [Arabidopsis thaliana] (TAIRAT3G06450.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO70569.1); contains
255025.at	AT4G09900	713	8.00	0.00002	5.66	0.00002	8.00	0.000002	hydrolase, alpha/beta fold family protein
262790.at	AT1G16390	713	6.06	0.00002	8.57	0.00002	6.96	0.000002	ATDCT3 (ARABIDOPSIS THALIANA ORGANIC CATION/CARNITINE TRANSPORTER2); carboxylate transmembrane transporter/ sugar/hydrogen i
263931.at	AT2G32220	713	6.96	0.00002	6.96	0.00002	6.96	0.000002	similar to unknown protein [Arabidopsis thaliana] (TAIRAT2G32220.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO15901.1)
245982.at	AT5G13170	696	9.19	0.00002	4.59	0.00006	7.46	0.000002	unknown protein
246036.at	AT5G08370	696	9.19	0.00002	6.50	0.00002	5.66	0.000002	ATAGAL2 (ARABIDOPSIS THALIANA ALPHA-GALACTOSIDASE 2); alpha-galactosidase
260544.at	AT2G43540	696	7.46	0.00002	5.66	0.00002	8.00	0.000002	similar to hypothetical protein [Vitis vinifera] (GB:CAN5294.1)
253066.at	AT4G37770	681	6.06	0.00002	4.59	0.00002	11.31	0.000002	ACS8 (1-Amino-cyclopropane-1-carboxylate synthase 8)
261580.at	AT1G01110	681	9.19	0.00002	3.73	0.00002	8.19	0.000114	IDO18 (IQ-domain 18)
261126.at	AT2G25920	681	5.66	0.00002	5.66	0.00002	10.56	0.000002	ectopic putative
267631.at	AT2S42150	681	11.31	0.000114	4.29	0.00002	6.50	0.000002	DNA-binding bromodomain-containing protein
264953.at	AT1G77120	681	13.93	0.00002	2.64	0.00002	8.57	0.000002	ADH1 (ALCOHOL DEHYDROGENASE 1)
251491.at	AT3G58480	665	5.66	0.00002	5.66	0.00002	9.19	0.000002	pH8-type carbohydrate kinase family protein
255911.at	AT1G66930	665	2.46	0.00249	9.19	0.004073	13.00	0.000307	serine/threonine protein kinase family protein
258300.at	AT3G23340	650	8.00	0.00002	7.46	0.00002	4.59	0.000002	CK1.10 (Casein Kinase I-like 10); casein kinase I/ kinase
253024.at	AT5G16270	650	6.50	0.00002	6.96	0.00023	6.96	0.000002	ANAC087; transcription factor
250671.at	AT5G06710	650	7.46	0.00002	6.06	0.00002	6.06	0.000002	similar to unknown protein [Arabidopsis thaliana] (TAIRAT2G38420.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO15955.1)
253165.at	AT4G35320	650	6.96	0.00002	6.96	0.00002	5.66	0.000002	similar to unknown protein [Arabidopsis thaliana] (TAIRAT2G17300.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN78386.1)
257483.at	AT1G49620	650	6.96	0.00002	7.46	0.00002	5.66	0.000002	ICK5/ICN6/KRP7 (KIP-RELATED PROTEIN 7); cyclin binding / cyclin-dependent protein kinase inhibitor
262188.at	AT1G77810	650	6.96	0.000035	5.66	0.000027	6.96	0.000023	galactosyltransferase family protein
264931.at	AT1G06590	650	11.31	0.00002	6.50	0.00002	3.73	0.000002	polygalacturonase, putative / pectinase, putative
267077.at	AT5G40970	650	6.96	0.00002	6.96	0.00002	5.66	0.000002	myb family transcription factor
261781.at	AT2G44210	650	6.96	0.00002	6.96	0.00002	6.96	0.000002	similar to unknown protein [Arabidopsis thaliana] (TAIRAT1G55360.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO87164.1); contains
249202.at	AT5G42580	635	8.57	0.00002	4.59	0.000088	6.50	0.000002	CYP705A12 (cytochrome P450, family 705, subfamily A, polypptide 12); oxygen binding
255964.at	AT1G22275	635	4.92	0.000078	21.11	0.000035	2.46	0.001832	ZYP1b
257469.at	AT1G49290	635	8.00	0.000241	4.92	0.000189	6.50	0.000078	similar to unknown protein [Arabidopsis thaliana] (TAIRAT5G13820.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN72326.1)
264226.at	AT1G06710	635	8.57	0.00002	6.06	0.00002	4.92	0.000002	leucine-rich repeat family protein
265291.at	AT2G42990	635	13.93	0.00002	3.83	0.00002	6.06	0.000023	QDSL-modII lipase/hydrolase family protein
246822.at	AT5G25960	620	4.00	0.000048	2.46	0.000037	24.25	0.000048	QDSL-modII lipase/hydrolase family protein
260565.at	AT2G43800	620	6.96	0.00002	5.28	0.00002	6.50	0.000002	formin homology 2 domain-containing protein / FH2 domain-containing protein
267181.at	AT2G37780	620	7.46	0.00002	5.28	0.000023	6.06	0.000002	aldo/keto reductase family protein
248253.at	AT5G53290	606	3.48	0.00002	10.56	0.000023	6.06	0.000002	CRF3 (CYTOKININ RESPONSE FACTOR 3); DNA binding / transcription factor
246019.at	AT5G10720	592	6.96	0.00002	6.50	0.00003	4.59	0.000002	AHK5 (CYTOKININ INDEPENDENT 2)
250173.at	AT5G14340	592	6.96	0.00002	4.59	0.000033	6.50	0.000002	AMV10 (myb domain protein 40); DNA binding / transcription factor
250802.at	AT5G04970	592	5.66	0.00004	14.83	0.00003	6.96	0.000026	pectinesterase, putative
253769.at	AT4G28560	592	5.66	0.00013	8.57	0.000307	4.59	0.000046	RC7 (ROP-INTERACTIVE CRIB MOTIF-CONTAINING PROTEIN 7); protein binding
256877.at	AT3G28470	592	6.06	0.00002	4.92	0.00002	6.96	0.000002	similar to ADRI-1 (ADRI-LIKE 1), ATP binding / protein binding [Arabidopsis thaliana] (TAIRAT4G33002.1); similar to ADRI-1 (ADRI-LIKE 1), AT
261953.at	AT1G64440	592	6.06	0.00002	6.96	0.00002	5.28	0.000002	RHD1 (ROOT HAIR DEFECTIVE 1); UDP-glucose 4-epimerase
246885.at	AT5G40680	592	6.50	0.00002	5.28	0.00002	6.06	0.000002	similar to unknown protein [Arabidopsis thaliana] (TAIRAT2G10930.1)
246885.at	AT5G40680	592	6.50	0.00002	5.28	0.00002	6.06	0.000002	transferase family protein
244489.at	AT5G36900	592	4.00	0.00002	4.92	0.000052	10.56	0.000002	ATP12G/PTR3/PEPTIDE TRANSPORTER PROTEIN 3); transporter
249323.at	AT5G46050	579	6.96	0.00002	4.29	0.00002	6.96	0.000002	ATAF1 (Arabidopsis NAC domain containing protein 2); transcription factor
261564.at	AT1G01120	579	4.59	0.00002	6.50	0.00002	6.50	0.000002	ATEX070H8 (exocyst subunit EXO70 family protein H8); protein binding
263439.at	AT2G28650	579	8.00	0.00002	3.73	0.00002	6.50	0.000002	ATDCH18 (cation/hydrogen exchanger 18); monovalent cation/proton antiporter
249255.at	AT5G41610	579	27.86	0.000023	1.87	0.000493	3.73	0.000027	similar to unknown protein [Arabidopsis thaliana] (TAIRAT2G38995.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO48523.1); contains
249614.at	AT5G37300	579	39.40	0.000046	2.30	0.000582	2.14	0.004073	AP2 domain-containing transcription factor family protein
260856.at	AT1G21910	579	3.25	0.00002	6.96	0.00002	8.57	0.000002	binding
250961.at	AT1G05990	579	6.96	0.00002	4.29	0.00002	5.28	0.000002	MUM4 (MUCLAGE-MODIFIED 4); catalytic
260865.at	AT1G53550	579	6.96	0.00002	5.66	0.00002	5.28	0.000002	leucine-rich repeat transmembrane protein kinase, putative
261434.at	AT1G07650	579	6.96	0.00002	4.92	0.00002	5.66	0.000002	transposable element gene
265979.at	AT2G11150	579	7.46	0.00023	7.46	0.00002	3.48	0.001077	aspartyl protease family protein
257897.at	AT3G12700	566	6.06	0.00002	4.59	0.00002	6.50	0.000002	heavy-metal-associated domain-containing protein
247394.at	AT5G06800	566	5.66	0.00002	4.29	0.000052	7.46	0.000002	similar to unknown protein [Arabidopsis thaliana] (TAIRAT5G06820.1)
250871.at	AT5G03950	566	8.57	0.000101	2.46	0.00002	5.28	0.000027	glycosyl hydrolase family 18 protein
254544.at	AT4G19820	566	6.50	0.00002	5.28	0.00003	5.66	0.000002	PGP9 (P-GLYCOPROTEIN 9); ATPase, coupled to transmembrane movement of substances
254710.at	AT4G18050	566	8.57	0.00002	3.03	0.00002	6.96	0.000021	similar to unknown [Populus trichocarpa] (GB:ABK94840.1)
261675.at	AT1G18290	566	3.48	0.000068	18.28	0.001336	2.83	0.000024	ATPME2 (Arabidopsis thaliana pectin methyltransferase 2)
262198.at	AT1G53830	566	5.66	0.00002	5.28	0.00002	6.06	0.000002	tropomyosin-related
262538.at	AT1G11740	566	6.06	0.00002	5.28	0.00002	5.66	0.000002	DRE5 (DSSRNA-BINDING PROTEIN 5); double-stranded RNA binding
246338.at	AT1G10710	566	6.06	0.00002	4.92	0.00002	6.96	0.000002	ATL2H2 (chlorophyll-chlorophyllide hydrolase 2)
246091.at	AT5G43660	553	6.96	0.000048	4.29	0.00002	6.50	0.000002	SLAH2 (SLAC1 HOMOLOGUE 2); transporter
253828.at	AT4G27970	553	5.66	0.00002	5.66	0.00002	5.28	0.000002	nodulin MN21 family protein
257300.at	AT3G28080	553	6.96	0.00002	4.29	0.00002	5.66	0.000002	similar to unknown protein [Arabidopsis thaliana] (TAIRAT3G54200.1); similar to plant cell wall protein SITFR88 [Lycopersicon esculentum] (GB:BF3
266596.at	AT2G46150	553	6.50	0.00002	4.29	0.00002	4.92	0.000002	zinc ion binding
246283.at	AT4G36860	553	6.50	0.00002	5.28	0.00002	4.92	0.000002	tetratricopeptide repeat (TPR)-containing protein
247229.at	AT5G08190	553	3.73	0.00002	9.19	0.00002	4.92	0.000101	periodic 17 (PER17.1) P17
264001.at	AT2G24200	553	8.00	0.00002	3.03	0.00002	6.96	0.000002	CKK3 (CYTOKININ OXIDASE 3); cytokinin dehydrogenase
247956.at	AT5G56970	540	5.28	0.00003	4.92	0.000046	6.50	0.000002	protein kinase, putative
249361.at	AT5G40540	540	5.28	0.00002	5.28	0.00002	5.66	0.000002	GRAM domain-containing protein / ABA-responsive protein-related
250279.at	AT5G13200	540	5.66	0.00002	4.00	0.00002	6.96	0.000002	MYB108 (MYB DOMAIN PROTEIN 108); DNA binding / transcription factor
258516.at	AT3G06490	540	5.28	0.00002	4.59	0.00013	6.50	0.000004	ML04 (MILDEW RESISTANCE LOCUS O 4); calmodulin binding
260483.at	AT1G11000	540	5.66	0.00002	4.92	0.00002	5.66	0.000002	ATA8C (METACASPASE 1); caspase
262723.at	AT1G11420	540	9.19	0.00002	3.48	0.000023	3.03	0.000068	SOCL23 (serine carboxypeptidase-like 23); serine carboxypeptidase
265655.at	AT2G24010	540	2.64	0.000533	18.70	0.000438	3.03	0.000002	curculin-like (mannose-binding) lectin family protein
249983.at	AT5G18470	528	6.50	0.00002	6.06	0.00002	7.46	0.000002	hydroxyproline-rich glycoprotein family protein
247958.at	AT5G57070	528	6.06	0.00002	6.06	0.00002	4.00	0.000002	similar to unknown protein [Arabidopsis thaliana] (TAIRAT5G06270.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO15841.1); similar to
249941.at	AT5G22270	528	4.29	0.00002	4.29	0.00002	8.00	0.000002	strobilactone synthase family protein
260398.at	AT1G40110	528	4.59	0.00002	3.73	0.00002	8.57	0.000002	endoglucanase/transucanase/glycohydrolase family protein
258011.at	AT2G37440	528	6.06	0.00004	6.50	0.00002	6.96	0.000002	ATPEN1 (PUTATIVE PENTACYCLIC TRITERPENE SYNTHASE 3); catalytic/ lipoel synthase
249687.at	AT5G25150	516	6.06	0.00013	2.30	0.001851	8.57	0.000023	NIC3 (NICOTINAMIDASE 3); catalytic/ nicotinamidase
249848.at	AT5G23220	516	6.50	0.00002	3.73	0.00002	5.66	0.000002	AMV56 (myb domain protein 56); DNA binding / transcription factor
250051.at	AT5G17800	516	7.46	0.000052	3.73	0.00002	4.92	0.000078	oxidoreductase, ZOG-Fe(II) oxygenase family protein
252530.at	AT3G46500	516	5.66	0.00002	6.06	0.00003	4.00	0.000006	Encodes a Gibberellin-regulated GASA/GAST/Slavin family protein
265331.at	AT2G18420	516	12.13	0.00003	1.87	0.005983	6.06	0.000035	protein kinase family protein
265405.at	AT2G18750	516	6.96	0.00002	5.66	0.00002	4.92	0.000002	AAO1 (ALDEHYDE OXIDASE 1)
246133.at	AT5G20960	504	4.59	0.00002	4.59	0.00002	6.06	0.000002	zinc finger (GATA type) family protein
251373.at	AT3G60530	504	4.00	0.00002	5.66	0.00002	5.66	0.000002	ETR2 (ETHYLENE RESPONSE 2); receptor
257922.at	AT3G23150	504	6.06	0.00002	4.00	0.000467	5.28	0.000002	transferase family protein
264403.at	AT2G25150	504	5.66	0.00002	3.73	0.000046	6.06	0.000023	acyl-fatty-carrier-protein desaturase, putative / stearyl-ACP desaturase, putative
264502.at	AT5G16240	492	4.92	0.00002	5.66	0.00002	4.29	0.000002	short-chain dehydrogenase/reductase (SDR) family protein
251013.at	AT5G02540	492	3.83	0.00002	4.92	0.00002	6.96	0.000027	auxin-responsive family protein
251291.at	AT3G61900	492	4.29	0.00002	4.59	0.00003	6.06	0.000002	MYB51 (MYB DOMAIN PROTEIN 51); DNA binding / transcription factor
255753.at	AT1G18570	492	4.29	0.00002	2.83	0.00002	9.85	0.000002	NLA (N

245628.at	AT1G56650	4.19	6.50	0.000078	3.48	0.001651	3.25	0.003355	PAP1 (PRODUCTION OF ANTHOCYANIN PIGMENT 1); DNA binding / transcription factor
247382.at	AT5G63410	4.19	6.06	0.00002	3.73	0.00002	3.25	0.00002	leucine-rich repeat transmembrane protein kinase, putative
248443.at	AT5G51310	4.19	4.00	0.00002	4.59	0.000023	4.00	0.00002	gibberellin 20-oxidase-related
248135.at	AT1G68400	4.19	3.48	0.000027	4.59	0.00002	4.00	0.00002	calmodulin-related protein, putative
245336.at	AT4G16151	4.19	4.92	0.00002	3.48	0.00002	4.29	0.00002	unknown protein
249747.at	AT5G24600	4.19	5.28	0.00002	2.83	0.000078	4.92	0.000023	similar to unknown protein [Arabidopsis thaliana] (TAIRAT3G18215.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO65983.1); contains 1 zinc finger (C3HC4-type RING finger) family protein
251066.at	AT5G01880	4.19	8.00	0.000052	2.46	0.000052	3.73	0.000088	HR4 (HOMOLOG OF RPW8 4)
252170.at	AT3G50480	4.19	3.48	0.00002	2.83	0.00003	7.46	0.000023	RD20 (RESPONSIVE TO DESSICATION 20); calcium ion binding
255795.at	AT2G33390	4.19	7.46	0.00002	2.84	0.00002	3.73	0.00002	SEC14 cytosolic factor, putative / phosphatidylinositol transferase protein, putative
281116.at	AT1G15370	4.19	4.92	0.00002	3.73	0.00002	4.29	0.00002	similar to unknown protein [Arabidopsis thaliana] (TAIRAT1G11700.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO11934.1); contains 1 zinc finger (C3HC4-type RING finger) family protein
248428.at	AT1G61830	4.19	4.92	0.00002	2.84	0.00002	4.29	0.00002	ATBAG2 (ARABIDOPSIS THALIANA BCL-2-ASSOCIATED ATHANOGENE 2)
245485.at	AT4G16230	4.09	5.28	0.000389	2.30	0.001832	5.66	0.000078	GDSL-motif lipase/hydrolase family protein
247461.at	AT5G62100	4.09	3.73	0.00002	4.59	0.00002	4.00	0.00002	HAT2 (ARABIDOPSIS THALIANA BCL-2-ASSOCIATED ATHANOGENE 2)
248801.at	AT5G47370	4.09	4.59	0.00002	3.48	0.00002	4.29	0.00002	antyrin repeat family protein
250201.at	AT5G14230	4.09	5.28	0.00002	2.83	0.00002	4.59	0.00002	similar to unknown protein [Arabidopsis thaliana] (TAIRAT2G27090.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO49895.1); contains 1 zinc finger (C3HC4-type RING finger) family protein
252695.at	AT4G39790	4.09	6.50	0.000066	3.48	0.000774	3.03	0.000066	microtubule-associated protein-related
252944.at	AT4G38320	4.09	4.59	0.00002	4.00	0.00002	3.73	0.00002	CYCD5.1 (CYCLIN D5.1); cyclin-dependent protein kinase
253055.at	AT4G37630	4.09	4.29	0.00002	4.00	0.00002	4.00	0.00002	ACS7 (1-Amino-cyclopropane-1-carboxylate synthase 7); 1-aminocyclopropane-1-carboxylate synthase
253999.at	AT4G28200	4.09	4.92	0.000088	2.64	0.00002	5.28	0.00002	28.5 kDa class P-related heat shock protein (HSP28.5-P)
254384.at	AT4G21870	4.09	4.29	0.00002	3.25	0.00002	4.92	0.00002	E12A11; phosphatidylethanolamine binding
256073.at	AT1G18100	4.09	9.19	0.000027	1.32	0.001486	5.66	0.00002	GDSL-motif lipase, putative
254949.at	AT1G31550	4.09	5.28	0.00002	3.48	0.00002	3.73	0.00002	galactosyltransferase family protein
257560.at	AT3G14960	4.09	3.73	0.00002	3.73	0.00002	4.92	0.00002	leucine-rich repeat transmembrane protein kinase, putative
258684.at	AT3G08680	4.09	5.28	0.00002	3.48	0.00002	3.73	0.00002	NHL2 (NDR1/HN1-like 2)
259071.at	AT3G11650	4.09	3.73	0.00002	3.73	0.00002	4.92	0.00002	C2 domain-containing protein
259222.at	AT3G03880	4.09	4.59	0.00002	3.73	0.00002	4.00	0.00002	ZOP37
262072.at	AT1G59590	4.09	2.83	0.00002	3.48	0.00002	6.96	0.00002	ATP2F-AB (Phloem protein 2-AB); transmembrane receptor
248979.at	AT5G46080	4.00	4.73	0.000027	4.29	0.000044	6.96	0.000023	Tol-interleukin-18 resistance (TIR) domain-containing protein
254691.at	AT5G45220	4.00	2.83	0.000027	3.25	0.000101	4.00	0.000024	exostosin family protein
251594.at	AT3G57630	4.00	4.59	0.00002	3.25	0.00002	4.29	0.00002	SOL1 (TSO1-Like); transcription factor
258326.at	AT3G22760	4.00	4.59	0.00002	3.48	0.00002	4.00	0.000068	CPK9 (CBL-INTERACTING PROTEIN KINASE 9); kinase
261581.at	AT1G01140	4.00	3.48	0.00002	4.00	0.00002	4.59	0.00002	nucleosporin family protein
262124.at	AT1G09660	4.00	4.00	0.000492	3.25	0.000088	4.92	0.000035	TUA1 (ALPHA-1/TUBULIN)
252855.at	AT1G64740	4.00	3.48	0.00002	3.73	0.00002	4.92	0.00002	ATPSK5 (PHYTOSULFONINE 5 PRECURSOR); growth factor
247109.at	AT5G56570	3.91	4.00	0.00002	4.29	0.00002	4.29	0.00002	JAA1/JAZ10/TFY9 (JASMONATE-ZIM-DOMAIN PROTEIN 10)
250929.at	AT5G13220	3.91	3.25	0.000046	2.46	0.000189	7.46	0.00002	IAA29 (indoleacetic acid-induced protein 29); transcription factor
253423.at	AT4G32280	3.91	3.25	0.00002	2.84	0.00002	4.00	0.000035	unknown protein
253827.at	AT4G28085	3.91	4.59	0.00002	2.14	0.00002	6.06	0.00002	cinnamoyl-CoA reductase
259975.at	AT1G76470	3.91	6.06	0.000023	2.00	0.000046	4.92	0.00002	similar to unknown protein [Arabidopsis thaliana] (TAIRAT5G18720.1); similar to unknown [Populus trichocarpa] (GB:ABK92464.1); similar to Osdg02
260182.at	AT1G10750	3.91	4.00	0.000027	3.48	0.000023	4.29	0.00002	similar to unknown protein [Arabidopsis thaliana] (TAIRAT3G18560.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN78728.1); similar to unkn
260754.at	AT1G49000	3.91	4.00	0.00002	2.46	0.00002	3.73	0.00002	calcium-dependent protein kinase, putative / GDP, putative
245136.at	AT2G45210	3.91	4.29	0.00002	4.00	0.00002	3.48	0.00002	transferase family protein
261605.at	AT1G49580	3.91	4.29	0.00002	4.00	0.00002	3.48	0.00002	transferase family protein
249494.at	AT5G39050	3.82	2.46	0.001486	3.48	0.000966	6.50	0.00002	CYCD3.3 (CYCLIN D3.3); cyclin-dependent protein kinase
252189.at	AT3G50070	3.82	4.00	0.00002	3.25	0.00002	4.29	0.00002	FAM1 (FERULATE-5-HYDROXYLASE 1); ferulate 5-hydroxylase
253088.at	AT4G36220	3.82	3.48	0.00002	3.73	0.00002	4.29	0.00002	ADL (ASPARTATE OXIDASE L)-aspartate oxidase
259197.at	AT3G29970	3.82	2.14	0.003355	4.00	0.00011	5.66	0.001336	ABL4 (ABL INTERACTOR-LIKE PROTEIN 4)
259986.at	AT1G68120	3.82	14.93	0.000307	1.74	0.001486	2.14	0.003355	SOPL48 (serine carboxypeptidase-like 48); serine carboxypeptidase
260924.at	AT1G21590	3.82	4.59	0.00002	3.25	0.00002	3.73	0.00002	RH3AB (RING-H2 finger A3B); protein binding / zinc ion binding
266637.at	AT2G35600	3.82	13.00	0.000438	1.87	0.000389	2.30	0.00002	ENP (ENHANCER OF PINOID); signal transducer
267498.at	AT2G45720	3.82	4.59	0.00002	3.25	0.00002	3.73	0.00002	armadillo/beta-catenin repeat family protein
245099.at	AT2G23000	3.82	4.92	0.000078	2.83	0.000027	4.00	0.000189	leucine-rich repeat transmembrane protein kinase, putative
246597.at	AT5G14760	3.82	4.59	0.00002	2.84	0.00002	3.73	0.00002	ADL (ASPARTATE OXIDASE L)-aspartate oxidase
248231.at	AT5G42030	3.82	4.59	0.00002	3.48	0.00002	3.48	0.00002	RH3AB (RING-H2 finger A3B); protein binding / zinc ion binding
252806.at	AT3G45010	3.82	4.00	0.00002	3.73	0.00002	3.73	0.00002	ENP (ENHANCER OF PINOID); signal transducer
253140.at	AT4G35480	3.82	4.00	0.00002	2.83	0.00002	4.92	0.00002	adenylyl sulfate kinase, putative
253493.at	AT4G31820	3.82	3.03	0.000023	3.25	0.00002	5.66	0.00002	adenylyl sulfate kinase, putative
254706.at	AT4G17950	3.82	4.29	0.00002	3.73	0.00002	3.48	0.00002	AP2 domain-containing transcription factor, putative
261471.at	AT1G14460	3.82	4.00	0.00002	4.00	0.00002	3.48	0.000046	DNA polymerase-related
266187.at	AT2G58970	3.82	4.59	0.00002	3.73	0.00002	3.25	0.00002	zinc finger (C3HC4-type RING finger) family protein
267425.at	AT2G34810	3.82	3.25	0.00002	4.29	0.00002	4.00	0.00002	FAD-binding domain-containing protein
247005.at	AT5G67520	3.73	3.73	0.000167	4.00	0.000052	3.48	0.000088	adenylyl sulfate kinase, putative
247041.at	AT5G67180	3.73	4.00	0.000023	4.00	0.00002	3.25	0.000048	AP2 domain-containing transcription factor, putative
247352.at	AT5G63850	3.73	4.29	0.00002	2.14	0.00002	4.59	0.00002	SNRK2.5/SRKN2.5/SRK2 (SNF1-RELATED PROTEIN KINASE 2.5); kinase
253554.at	AT4G30940	3.73	2.64	0.000114	2.83	0.000114	5.66	0.00003	potassium channel tetramerization domain-containing protein
253796.at	AT4G26460	3.73	3.65	0.000101	2.14	0.00003	9.19	0.00002	unknown protein
254015.at	AT4G26140	3.73	5.28	0.00002	2.83	0.00002	3.48	0.00002	BGAL12 (beta-galactosidase 12); beta-galactosidase
258037.at	AT3G21230	3.73	4.29	0.00002	3.03	0.00002	4.00	0.00002	4CL5 (4-COUMARATE-COA LIGASE 5); 4-coumarate-CoA ligase
260068.at	AT1G73805	3.73	2.00	0.00002	4.00	0.00003	6.50	0.00002	calmodulin binding
262181.at	AT1G78090	3.73	4.59	0.00002	3.48	0.00002	3.25	0.00002	glycosyl hydrolase family 3 protein
262999.at	AT1G15100	3.73	4.59	0.00002	3.48	0.00002	3.25	0.00002	RH2A (RING-H2 finger A2A); protein binding / zinc ion binding
265983.at	AT2G24260	3.73	4.8	0.00002	3.48	0.00002	3.48	0.00002	basic helix-loop-helix (bHLH) family protein
250302.at	AT5G11820	3.73	4.00	0.000101	2.46	0.000052	5.28	0.00004	ATOWNIV6 (6-81-FRUITAN EXOHYDROLASE); hydrolase, hydrolyzing O'-glycosyl compounds / inulinase / levanase
251683.at	AT3G57120	3.73	3.73	0.00002	2.83	0.00002	4.92	0.00002	protein kinase family protein
254594.at	AT4G18930	3.65	4.29	0.00002	3.48	0.00002	3.25	0.00002	cyclic phosphodiesterase
262983.at	AT1G15110	3.65	4.29	0.00002	3.48	0.00002	3.25	0.00002	phosphatidyl serine synthase family protein
246922.at	AT5G25110	3.65	3.03	0.00002	4.29	0.00002	3.73	0.00002	CPK25 (CBL-INTERACTING PROTEIN KINASE 25); kinase
249092.at	AT5G43710	3.65	3.48	0.00002	3.73	0.00002	3.73	0.00002	glycosyl hydrolase family 47 protein
249115.at	AT5G43810	3.65	3.73	0.00002	3.25	0.00002	4.00	0.00002	ZLL (ZWILLE)
253779.at	AT4G28490	3.65	4.29	0.00002	2.14	0.000078	5.28	0.00002	HAESA (RECEPTOR-LIKE PROTEIN KINASE 5); ATP binding / kinase / protein serine/threonine kinase
258078.at	AT3G25870	3.65	4.59	0.00002	3.73	0.000023	2.83	0.00002	similar to unknown protein [Arabidopsis thaliana] (TAIRAT1G13360.1); similar to unknown [Populus trichocarpa] (GB:ABK92948.1)
258107.at	AT3G23560	3.65	3.73	0.000088	2.83	0.00002	4.59	0.00002	ALF5 (ABERRANT LATERAL ROOT FORMATION 5); antiporter / transporter
259329.at	AT3G26320	3.65	4.00	0.00002	3.73	0.00006	3.25	0.00002	similar to unnamed protein product [Vitis vinifera] (GB:CAO44440.1)
260529.at	AT4G17260	3.65	3.73	0.00002	2.83	0.00002	4.29	0.00002	WRKY2 (WRKY DNA-binding protein 23); transcription factor
264019.at	AT2G21130	3.65	3.73	0.00002	3.03	0.00002	4.29	0.00002	pepsidyl-prolyl cis-trans isomerase / cyclophilin (CYP2) / rotamase
248558.at	AT5G49990	3.56	4.59	0.00002	3.25	0.00002	3.03	0.000114	xanthine/uracil permease family protein
252557.at	AT3G45960	3.56	5.66	0.000027	2.14	0.00006	3.73	0.000389	ATEXLA3 (ARABIDOPSIS THALIANA EXPANSIN-LIKE A3)
253815.at	AT4G28250	3.56	4.59	0.00002	4.00	0.00002	2.46	0.00002	ATEXPB3 (ARABIDOPSIS THALIANA EXPANSIN B3)
261400.at	AT1G79830	3.56	4.00	0.00002	3.25	0.00002	3.48	0.00002	protein phosphatase 2C family protein / PP2C family protein
262782.at	AT1G13195	3.56	3.48	0.00002	3.03	0.00005	4.29	0.00004	zinc finger (C3HC4-type RING finger)

287305.at	AT2G30070	3.17	3.48	0.00002	2.83	0.00002	3.25	0.00002	ATKT1 (Arabidopsis thaliana K <sup>+</sup> uptake 1); potassium ion transmembrane transporter
287411.at	AT2G34930	3.17	4.29	0.00002	3.25	0.00003	3.70	0.00002	disease resistance family protein
287473.at	AT2G47520	3.10	2.64	0.00014	3.03	0.00003	3.30	0.00002	AP2 domain-containing transcription factor, putative
287495.at	AT2G28410	3.10	3.25	0.00002	2.83	0.00002	3.25	0.00002	UBI1 (UBUSTIN-COMJUGATING ENZYME 17); ubiquitin-protein ligase
288225.at	AT5G47130	3.10	3.48	0.00017	2.14	0.00013	4.00	0.00002	Bax inhibitor-1 family / BH-1 family
249618.at	AT5G37490	3.10	2.46	0.000692	2.46	0.00249	4.92	0.00002	U-box domain-containing protein
253378.at	AT4G33310	3.10	2.64	0.000618	5.28	0.00304	2.14	0.00189	unknown protein
259252.at	AT1G12570	3.10	4.59	0.000214	2.46	0.000035	2.64	0.000389	glucose-methanol-choline (GMC) oxidoreductase family protein
261296.at	AT1G28770	3.10	3.25	0.00002	3.03	0.00002	3.03	0.00002	ATEXP10 (ARABIDOPSIS THALIANA EXPANSIN A10)
262225.at	AT1G28990	3.10	3.64	0.000023	3.48	0.000023	3.48	0.000023	similar to unnamed protein product [Vitis vinifera] (GB:CA065660.1); contains InterPro domain Methyltransferase F4M (InterPro:IPR006342)
264385.at	AT1G12020	3.10	2.74	0.00002	2.46	0.00002	3.25	0.00002	similar to unnamed protein product [Vitis vinifera] (GB:CA065660.1); contains InterPro domain Methyltransferase F4M (InterPro:IPR006342)
264588.at	AT2G17730	3.10	2.83	0.000068	2.46	0.000035	4.29	0.00003	zinc finger (C2HC4-type RING finger) family protein
264824.at	AT1G03420	3.10	3.25	0.00002	3.25	0.00002	2.83	0.00008	transposable element gene
265993.at	AT2G24160	3.10	4.29	0.000035	2.46	0.000088	2.83	0.00002	pseudogene, leucine rich repeat protein family, contains leucine rich repeat domains Pfam-PF0560, InterPro:IPR001611; contains some similarity t
267676.at	AT2G26680	3.10	3.73	0.00002	3.03	0.00002	2.64	0.00002	similar to unnamed protein product [Vitis vinifera] (GB:CA065660.1); contains InterPro domain Methyltransferase F4M (InterPro:IPR006342)
246268.at	AT1G31850	3.03	3.73	0.00002	2.46	0.00002	3.03	0.00002	dehydration-responsive protein, putative
247048.at	AT5G66440	3.03	3.03	0.00002	3.03	0.000027	3.03	0.000023	similar to unnamed protein [Arabidopsis thaliana] (TAIRAT4G24560.1); similar to hypothetical protein [Thellungiella halophila] (GB:ABB45849.1)
249370.at	AT5G40710	3.03	3.25	0.00002	2.83	0.00002	3.03	0.00002	zinc finger (C2H2 type) family protein
259864.at	AT1G72800	3.03	2.83	0.001201	1.62	0.000147	6.06	0.000023	nuM1-related
246498.at	AT5G16230	3.03	3.48	0.00002	2.46	0.000088	3.25	0.000023	acyl-(acyl-carrier-protein) desaturase, putative / stearoyl-ACP desaturase, putative
247186.at	AT5G65470	3.03	3.48	0.00002	2.46	0.00002	3.25	0.00002	similar to unnamed protein [Arabidopsis thaliana] (TAIRAT4G24530.1); similar to unnamed protein product [Vitis vinifera] (GB:CA061608.1); similar to
248096.at	AT5G55490	3.03	3.48	0.000046	2.00	0.00161	4.00	0.001077	ATCEX1/GE1 (GAEMTE EXPRESSED PROTEIN)
248295.at	AT5G53030	3.03	3.73	0.00023	2.30	0.00002	3.25	0.000389	similar to unnamed protein [Arabidopsis thaliana] (TAIRAT4G227810.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN71155.1)
254573.at	AT4G18420	3.03	2.30	0.00002	3.25	0.00002	3.73	0.00002	pectinacetylesterase family protein
260364.at	AT1G70560	3.03	3.73	0.00002	3.03	0.00002	2.46	0.00002	allinase C-terminal domain-containing protein
261804.at	AT1G30530	3.03	4.00	0.00002	2.64	0.00002	2.64	0.00002	UDP-glucuronosyl/UDP-glucosyl transferase family protein
263482.at	AT2G03980	3.03	2.83	0.00002	3.03	0.00002	3.25	0.00002	GDSL-motif lipase/hydrolase family protein
263967.at	AT2G36270	3.03	3.25	0.000042	2.30	0.000025	3.73	0.00003	ABS (ABA INSENSITIVE 5); DNA binding / transcription activator / transcription factor
264222.at	AT4G28900	2.96	2.64	0.000438	3.03	0.000088	3.03	0.00002	RAP210 (related to AP2 10); DNA binding / transcription factor
246911.at	AT2G58510	2.96	3.03	0.00002	3.73	0.00002	2.30	0.000035	TNY (TNY); DNA binding / transcription factor
251722.at	AT3G58200	2.96	3.25	0.00002	2.30	0.000114	3.48	0.00002	amino acid transporter family protein
252991.at	AT4G38470	2.96	2.46	0.00002	2.64	0.00002	4.00	0.00002	protein kinase family protein
253732.at	AT4G29140	2.96	3.03	0.00002	2.83	0.00002	3.03	0.00002	MATE efflux protein-related
254704.at	AT4G18020	2.96	3.73	0.000068	2.46	0.000035	2.83	0.000013	APRR2 (IPSEUDO-RESPONSE REGULATOR 2); transcription factor
257610.at	AT3G12810	2.96	2.83	0.00002	2.03	0.00002	3.03	0.00002	ATDD11 (ARABIDOPSIS THALIANA INDETERMINATE11); nucleic acid binding / transcription factor / zinc ion binding
257636.at	AT3G26200	2.96	1.74	0.000966	2.14	0.000307	6.96	0.000101	CYP71B22 (cytochrome P450, family 71, subfamily B, polypeptide 22); oxygen binding
258998.at	AT3G01820	2.96	2.83	0.00002	3.03	0.00002	3.03	0.00002	adenylate kinase family protein
259109.at	AT3G05880	2.96	3.48	0.000273	2.46	0.000088	3.03	0.000307	serine/threonine protein phosphatase, putative
262105.at	AT1G02810	2.96	3.25	0.00002	2.30	0.00002	3.48	0.00002	pectinesterase family protein
263953.at	AT3G26050	2.96	2.46	0.000147	2.46	0.000241	4.29	0.00003	ATOPF3 (OPF3) (Arabidopsis thaliana ovate family protein 15)
264033.at	AT1G28960	2.96	4.29	0.00002	2.46	0.000025	2.96	0.000088	zinc finger (C2HC4-type RING finger) family protein
264358.at	AT2G32280	2.96	3.25	0.00002	2.46	0.00002	3.25	0.00004	similar to unnamed protein [Arabidopsis thaliana] (TAIRAT4G221310.1); similar to unknown [Populus trichocarpa] (GB:ABX92874.1); contains InterPro c
266761.at	AT2G47130	2.96	2.83	0.00002	2.30	0.00002	4.00	0.00002	short-chain dehydrogenase/reductase (SDR) family protein
267339.at	AT2G39870	2.96	2.83	0.00002	3.25	0.00002	2.83	0.00002	similar to unnamed protein [Arabidopsis thaliana] (TAIRAT3G55690.1); similar to unnamed protein product [Vitis vinifera] (GB:CA069095.1)
259904.at	AT1G74150	2.96	2.64	0.000273	3.25	0.000046	3.03	0.000068	similar to unnamed protein [Arabidopsis thaliana] (TAIRAT3G55690.1); similar to unnamed protein product [Vitis vinifera] (GB:CA069095.1)
266778.at	AT2G26090	2.96	3.03	0.00002	3.25	0.000078	2.64	0.000101	CYP707A2 (cytochrome P450, family 707, subfamily A, polypeptide 2); oxygen binding
257105.at	AT3G15300	2.96	4.29	0.00002	2.46	0.000035	2.96	0.000068	VQ motif-containing protein
258700.at	AT3G09710	2.89	4.29	0.000046	2.46	0.000114	2.30	0.000052	IQD1 (IQ-DOMAIN 1); calmodulin binding
245965.at	AT5G19730	2.89	4.29	0.00002	3.25	0.00002	1.74	0.00013	pectinesterase family protein
246932.at	AT5G25190	2.89	3.25	0.00003	2.64	0.000167	2.83	0.000101	ethylene-responsive element-binding protein, putative
246953.at	AT5G04850	2.89	3.03	0.00002	2.83	0.00002	2.83	0.00002	VPS80.2
247178.at	AT5G65890	2.89	2.46	0.000078	2.83	0.00002	2.46	0.000101	AGR1 (ACT DOMAIN REPEAT 1)
247705.at	AT5G09550	2.89	2.46	0.00002	2.30	0.00002	3.48	0.00002	zinc finger (C2HC4-type RING finger) family protein
250277.at	AT5G12940	2.89	3.73	0.00002	2.46	0.00002	2.64	0.000088	leucine-rich repeat family protein
253670.at	AT4G29610	2.89	4.59	0.00002	2.64	0.000214	2.00	0.000202	cytidine deaminase, putative / cytidine aminohydrolase, putative
254562.at	AT4G19230	2.89	3.25	0.00002	2.46	0.00002	3.03	0.00002	CYP707A1 (cytochrome P450, family 707, subfamily A, polypeptide 1); oxygen binding
254821.at	AT4G18800	2.89	3.25	0.00003	2.83	0.00002	2.64	0.00002	WAP5 (WASP) (WISSKOTT-ALDRICH SYNDROME PROTEIN) FAMILY VERPULFON HOMOLOGOUS PROTEIN 5)
259042.at	AT3G21310	2.89	3.73	0.00006	2.46	0.000035	2.64	0.00004	similar to unnamed protein [Arabidopsis thaliana] (TAIRAT1G51770.1); similar to unnamed protein product [Vitis vinifera] (GB:CA045744.1); contains 1
258145.at	AT3G18200	2.89	3.25	0.00002	2.83	0.00002	2.46	0.00002	roadin (RD1) family protein
263325.at	AT2G04240	2.89	2.83	0.00002	2.83	0.00002	3.03	0.00002	XERD1; protein binding / zinc ion binding
267037.at	AT2G38320	2.89	2.46	0.00002	3.73	0.001201	2.64	0.00003	similar to unnamed protein [Arabidopsis thaliana] (TAIRAT5G01620.2); similar to unnamed protein [Arabidopsis thaliana] (TAIRAT5G01620.1); similar t
267423.at	AT2G35060	2.89	2.64	0.00002	2.64	0.00002	3.48	0.00002	KUP11 (K <sup>+</sup> uptake permease 11); potassium ion transmembrane transporter
248881.at	AT5G48900	2.83	3.03	0.00002	2.30	0.00002	3.25	0.00002	pectate lyase family protein
248808.at	AT5G47510	2.83	9.19	0.00002	1.52	0.001832	1.062	0.002733	SEC14 cytosolic factor family protein / phosphoglycerate transfer family protein
248921.at	AT5G47070	2.83	2.83	0.00002	2.30	0.00002	2.96	0.00002	protein kinase, putative
249043.at	AT5G41140	2.83	2.64	0.00002	2.83	0.00002	2.83	0.00003	similar to unnamed protein [Arabidopsis thaliana] (TAIRAT1G63300.1); similar to unnamed protein product [Vitis vinifera] (GB:CA062788.1); contains i
253084.at	AT4G36260	2.83	2.00	0.000273	2.46	0.003355	4.92	0.000088	STY2 (STYLISH 2)
253562.at	AT4G31130	2.83	3.03	0.00002	2.30	0.00002	3.25	0.00002	similar to hypothetical protein [Vitis vinifera] (GB:CAN84246.1); contains InterPro domain Protein of unknown function DUF1218 (InterPro:IPR090086)
255538.at	AT4G01880	2.83	3.03	0.00002	2.64	0.00002	2.83	0.00002	MYB55 (myb domain protein 55); DNA binding / transcription factor
255783.at	AT1G16730	2.83	4.29	0.000068	1.87	0.001486	2.83	0.000241	similar to unknown [Picea sitchensis] (GB:ABX21208.1)
257137.at	AT1G62890	2.83	2.64	0.00002	2.64	0.00002	3.25	0.00002	ATMDR11 (ATPG18/MDR1/MDR11); PGP19 (P-GLYCOPROTEIN 19); ATPase, coupled to transmembrane movement of substances / auxin efflux tr
258366.at	AT2G14230	2.83	2.64	0.00002	2.64	0.00002	2.64	0.00002	RAP210 (related to AP2 10); DNA binding / transcription factor
259737.at	AT1G64400	2.83	2.64	0.00002	2.30	0.00002	3.73	0.00002	long-chain-fatty-acyl-CoA ligase, putative / long-chain acyl-CoA synthetase, putative
260167.at	AT1G71970	2.83	3.03	0.00002	2.30	0.00002	3.25	0.00002	similar to unnamed protein [Arabidopsis thaliana] (TAIRAT1G22880.1); similar to unknown [Populus trichocarpa] (GB:ABX84468.1)
263959.at	AT2G01890	2.83	2.46	0.00002	3.03	0.00002	3.03	0.00002	PAP8 (PURPLE ACID PHOSPHATASE PRECURSOR); acid phosphatase / protein serine/threonine phosphatase
263920.at	AT2G36410	2.83	2.46	0.00002	2.46	0.00002	3.25	0.00002	similar to unnamed protein [Arabidopsis thaliana] (TAIRAT3G5920.1); similar to unknown [Populus trichocarpa] (GB:ABX83998.1); contains InterPro c
265117.at	AT1G62500	2.83	3.25	0.00002	2.83	0.00002	2.83	0.00002	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein
265385.at	AT2G20900	2.83	3.25	0.00002	2.30	0.00002	2.96	0.00002	diacylglycerol kinase, putative
266322.at	AT2C46690	2.83	2.83	0.00002	3.48	0.00002	2.30	0.00002	auxin-responsive family protein
266532.at	AT2G16890	2.83	3.73	0.00002	2.46	0.00002	2.46	0.00002	UDP-glucuronosyl/UDP-glucosyl transferase family protein
266802.at	AT2G22900	2.83	3.25	0.00002	2.46	0.00002	2.83	0.00002	galactosyl transferase GMA12/MNN10 family protein
245151.at	AT2G47550	2.76	2.46	0.00002	2.64	0.00002	3.25	0.00002	pectinesterase family protein
245840.at	AT1G69420	2.76	2.64	0.00114	1.62	0.005499	4.92	0.000023	similar to unnamed protein [Arabidopsis thaliana] (TAIRAT1G10140.1); contains InterPro domain Uncharacterised conserved protein UCP931279 (Inter
247965.at	AT5G55640	2.76	2.46	0.00002	3.48	0.00002	4.29	0.00002	AGP4 (ARABIDOPSIS GELATINASE 4)
248313.at	AT5G41560	2.76	3.03	0.00002	2.46	0.00002	2.83	0.00002	similar to unnamed protein product [Vitis vinifera] (GB:CA069907.1)
254796.at	AT4G13000	2.76	3.03	0.000865	2.14	0.000052	3.25	0.000101	protein kinase family protein
254810.at	AT4G12390	2.76	3.48	0.00002	2.46	0.00002	2.46	0.00002	PME1; pectinesterase inhibitor
256093.at	AT1G20923	2.76	3.73	0.00002	2.30	0.00002	2.46	0.000078	zinc finger (C2HC4-type RING finger) family protein
262703.at	AT1G16510	2.76	3.03	0.000023	2.83	0.00002	2.46	0.00002	DC1 domain-containing protein
262786.at	AT1G10740	2.76	2.83	0.00002	2.14	0.00002	3.48	0.00002	SNM1 (SENSITIVE TO NITROGEN MUSTARD 1)
263157.at	AT1G54100	2.76	2.64	0.00002	2.46	0.00002	3.25	0.00002	ALDH18A (ALDEHYDE DEHYDROGENASE 78A); 3-chloroethyl aldehyde dehydrogenase
268593.at	AT2G46200	2.76	3.03	0.00002	2.00	0.00002	3.48	0.00002	similar to unnamed protein product [Vitis vinifera] (GB:CA039889.1)
268606.at	AT2G46310	2.76	2.46	0.00003	2.83	0.00002	3.03	0.00002	ORF5 (CYTOKININ RESPONSE FACTOR 5); DNA binding / transcription factor
267839.at	AT2G42200	2.76	3.48	0.00003	2.30	0.00003	2.64	0.00013	squamosa promoter-binding protein-like 9 (SPB9)
248236.at	AT5G53870	2.70	2.14	0.001077	4.29	0.001077	2.14	0.000346	plastoquinone-like

252153.at	AT3G51360	258	3.73	0.00013	2.14	0.000101	2.14	0.001077	aspartyl protease family protein
252956.at	AT4G28580	258	3.48	0.00002	2.30	0.00002	2.14	0.000002	ATFP6 (FARNESYLATED PROTEIN 6); metal ion binding
253182.at	AT4G28190	258	2.46	0.000035	1.87	0.000355	3.73	0.000008	similar to unknown protein [Arabidopsis thaliana] (TAIRAT4G28190.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO47480.1); contains 1
253766.at	AT3G16260	258	3.25	0.00002	2.64	0.00002	2.64	0.000002	arabinoxylan inhibitor/sieve sterosyl transfer protein (LTP) family protein
253702.at	AT3G23750	258	2.46	0.00002	2.46	0.00002	2.83	0.000002	leucine-rich repeat family protein / protein kinase family protein
258357.at	AT3G14350	258	3.48	0.00002	2.46	0.00008	2.00	0.000002	SRF7 (STRUBBELIG-RECEPTOR FAMILY 7); ATP binding / protein serine/threonine kinase
258921.at	AT3G10500	258	2.30	0.00002	2.00	0.00002	3.73	0.000002	ANAC053 (Arabidopsis NAC domain containing protein 53); transcription factor
259967.at	AT1G76510	258	2.64	0.00002	2.30	0.000035	2.83	0.000002	ARID/BRIGHT DNA-binding domain-containing protein
260422.at	AT1G68150	258	2.83	0.00003	2.00	0.00002	3.03	0.000002	WRKY9 (WRKY DNA-binding protein 9); transcription factor
260939.at	AT1G64880	258	2.64	0.00003	2.64	0.00003	2.83	0.000046	zinc finger (C3HC4-type RING finger) family protein
260974.at	AT1G53440	258	2.64	0.00003	2.30	0.00002	2.83	0.000004	leucine-rich repeat family protein / protein kinase family protein
264026.at	AT2G21060	258	3.03	0.00002	2.14	0.00002	2.64	0.00003	ATRP2B (GLYCINE-RICH PROTEIN 2B); nucleic acid binding
265284.at	AT2G20230	258	2.64	0.00002	2.46	0.00002	2.64	0.00003	similar to unknown protein [Arabidopsis thaliana] (TAIRAT4G28770.1); similar to unknown [Populus trichocarpa] (GB:ABK3408.1); similar to unknown
266117.at	AT2G02170	258	2.46	0.000035	2.46	0.00003	2.83	0.000004	remorin family protein
266167.at	AT3G28860	258	3.03	0.00002	1.62	0.00002	3.48	0.000002	YL55 (yellow-leaf-specific gene 5)
245229.at	AT4G31970	252	2.46	0.00003	1.62	0.00002	3.48	0.000003	transposon-like repetitive DNA element
249770.at	AT5G24110	252	1.74	0.005408	1.87	0.00027	4.82	0.000002	WRKY30 (WRKY DNA-binding protein 30); transcription factor
249994.at	AT5G18590	252	2.46	0.00002	2.46	0.00002	2.64	0.000002	kelch repeat-containing protein
251009.at	AT5G02640	252	2.83	0.00006	2.46	0.00018	2.30	0.000273	similar to unknown protein [Arabidopsis thaliana] (TAIRAT3G46300.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN66778.1)
251826.at	AT3G55110	252	3.03	0.000101	2.14	0.00006	2.46	0.000046	ABC transporter family protein
253632.at	AT4G30430	252	2.30	0.000492	3.03	0.000389	2.30	0.000865	TE9 (TETRASPANIN9)
253989.at	AT4G28150	252	2.83	0.00002	2.14	0.00002	2.64	0.000002	similar to unknown protein [Arabidopsis thaliana] (TAIRAT5G58900.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN72576.1)
256586.at	AT3G20180	252	2.83	0.00002	2.46	0.00002	2.30	0.000002	BRX02/2 (BRASSINOSTEROID-6-OXIDASE 2); monoxygenase/ oxygen binding
256664.at	AT3G12040	252	2.46	0.000035	2.30	0.00003	2.83	0.000052	DNA-3-methyladenine glycosylase (MAG)
258462.at	AT3G17350	252	3.25	0.00002	2.30	0.00027	2.14	0.000273	similar to unknown protein [Arabidopsis thaliana] (TAIRAT5G50290.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO70913.1); contains 1
260395.at	AT1G69780	252	2.64	0.00002	3.03	0.00002	2.00	0.000003	ATH13; DNA binding / transcription factor
260800.at	AT1G78240	252	2.46	0.00006	2.14	0.00002	3.03	0.000002	TS02 (TUMOROUS SHOOT DEVELOPMENT 2); methyltransferase
260840.at	AT1G28090	252	3.03	0.00002	2.14	0.00002	2.46	0.000101	similar to unknown protein [Arabidopsis thaliana] (TAIRAT4G28470.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO48076.1); contains 1
261425.at	AT1G18920	252	2.83	0.00002	2.00	0.00002	2.64	0.000002	proton-dependent oligopeptide transport (POT) family protein
264692.at	AT1G70000	252	3.25	0.00002	2.14	0.00003	2.30	0.000618	DNA-binding family protein
264898.at	AT1G23205	252	3.03	0.00002	2.64	0.00002	2.00	0.000078	invertase/pectin methyltransferase inhibitor family protein
247519.at	AT5G61430	246	5.28	0.00023	1.52	0.004073	1.87	0.000101	ANAC100/ATNACS (Arabidopsis NAC domain containing protein 100); transcription factor
247628.at	AT5G60400	246	2.14	0.00002	2.64	0.00002	2.64	0.000002	unknown protein
249125.at	AT5G43380	246	2.64	0.00013	1.74	0.00048	3.25	0.000013	TOPP6 (Type one serine/threonine protein phosphatase 6); protein serine/threonine phosphatase
251010.at	AT5G25550	246	3.25	0.00002	2.14	0.00002	2.14	0.000002	unknown protein
254445.at	AT4G20930	246	2.83	0.00002	3.03	0.00002	1.74	0.000023	3-hydroxyisobutyrate dehydrogenase, putative
258818.at	AT3G21420	246	4.29	0.00003	1.52	0.00088	2.30	0.000078	oxidoreductase, 2OG-Fe(II) oxygenase family protein
258855.at	AT3G02070	246	2.30	0.00002	2.14	0.00002	3.03	0.000002	OTU-like cysteine protease family protein
258868.at	AT3G03110	246	2.14	0.00002	2.64	0.000273	2.64	0.000052	XPO1B (exportin 1B); protein transporter
259149.at	AT3G10340	246	2.64	0.00002	1.74	0.00048	3.25	0.000002	phenylalanine ammonia-lyase, putative
259686.at	AT1G27960	246	2.30	0.00002	2.14	0.00002	2.64	0.000014	ECT3 (evolutionarily conserved C-terminal region 3)
260001.at	AT1G67800	246	2.83	0.00002	1.74	0.00027	2.46	0.000002	similar to catalytic [Arabidopsis thaliana] (TAIRAT1G24350.1); similar to unknown [Picea sitchensis] (GB:ABK28930.1); contains InterPro domain Acid
260220.at	AT1G74650	246	2.64	0.000078	1.87	0.00148	3.03	0.000273	AIMY31/AY13 (myb domain protein 31); DNA binding / transcription factor
260540.at	AT2G43500	246	2.83	0.00002	1.87	0.00014	2.83	0.000035	RWP-RK domain-containing protein
261114.at	IGT5390AT1G75	246	3.73	0.00002	1.87	0.00006	2.14	0.000002	[AT1G7590, AT2B3P4 (ARABIDOPSIS THALIANA BASIC LEUCINE-ZIPPER 44); DNA binding / protein heterodimerization/transcription factor][A
263419.at	AT2G17220	246	2.46	0.00002	2.00	0.00002	3.03	0.000002	protein kinase family protein
263775.at	AT2G6410	246	2.83	0.00002	3.03	0.00023	1.74	0.000014	CP2 (GARRICE); DNA binding / transcription factor
267602.at	AT2S29270	246	2.14	0.00008	2.64	0.00002	2.64	0.000002	similar to unnamed protein product [Vitis vinifera] (GB:CAO24057.1)
257644.at	AT3G25780	246	2.64	0.00002	1.82	0.00002	3.48	0.000002	AOC3 (ALLENE OXIDE CYCLASE 3)
247569.at	AT5G81240	241	2.64	0.00002	2.14	0.00002	2.46	0.000002	protein binding
247930.at	AT5G57060	241	2.14	0.00002	2.30	0.00002	2.83	0.000002	similar to unknown protein [Arabidopsis thaliana] (TAIRAT4G28060.1); similar to unknown [Picea sitchensis] (GB:ABK23978.1); contains InterPro dom
251879.at	AT3G54200	241	2.30	0.00002	2.30	0.00003	2.64	0.000002	similar to unknown protein [Arabidopsis thaliana] (TAIRAT3G59575.1); similar to Herpin-induced 1 [Medicago truncatula] (GB:ABE93043.1); contains 1
254503.at	AT4G19120	241	2.83	0.00002	2.14	0.00002	2.64	0.000002	ERK2 (ERK1/2-RELATED KINASE 2); protein kinase
254791.at	AT4G12910	241	2.83	0.00003	2.14	0.00035	2.30	0.000002	SCPL29 (serine carboxypeptidase-like 29); serine carboxypeptidase
254922.at	AT4G11370	241	2.64	0.000046	1.74	0.00046	3.03	0.000002	RHA1A (RING-H2 finger A1A); protein binding / zinc ion binding
255134.at	AT4G08330	241	2.30	0.00027	2.30	0.00032	2.64	0.000003	Identical to Uncharacterized protein At4G08330, chloroplast precursor [Arabidopsis Thaliana] (GB:Q5STNS); similar to peptide-methionine ('S')-S-oxide
256020.at	AT1G58290	241	2.00	0.00002	1.87	0.00002	3.73	0.000002	HEMA1; glutamyl-tRNA reductase
259900.at	AT3G24670	241	2.46	0.00002	2.30	0.00002	2.46	0.000002	pectate lyase family protein
259819.at	AT3G64860	241	2.46	0.00002	1.74	0.00002	3.25	0.000002	EM4 (ETHYLENE INSENSITIVE 4); receptor
259933.at	AT1G12530	241	2.41	0.00027	2.30	0.00052	2.80	0.000033	similar to unknown protein [Arabidopsis thaliana] (TAIRAT1G56420.1); similar to OsD3g228500 [Oryza sativa (aponica cultivar-group)] (GB:NP_0010
260255.at	AT1G74330	241	1.87	0.000167	2.00	0.00341	3.73	0.000008	ATP binding / protein kinase
260264.at	AT1G68500	241	2.14	0.00023	2.83	0.00027	2.30	0.000002	similar to hypothetical protein [Vitis vinifera] (GB:CAN86643.1)
260783.at	AT1G06160	241	2.14	0.00002	1.74	0.00004	3.73	0.000002	ethylene-responsive factor, putative
260807.at	AT1G78310	241	2.00	0.00007	2.64	0.00002	2.64	0.000002	VG motif-containing protein
260933.at	AT1G62470	241	2.00	0.00007	2.00	0.00014	2.64	0.000002	similar to unknown protein [Arabidopsis thaliana] (TAIRAT1G02475.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO46177.1); contains 1
263545.at	AT2G21560	241	2.83	0.00002	2.83	0.00002	1.74	0.000552	similar to unknown protein [Arabidopsis thaliana] (TAIRAT4G28160.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN71202.1)
263594.at	AT2G01880	241	2.83	0.00002	2.46	0.00002	2.00	0.000002	ATPAP7/PAP7 (purple acid phosphatase 7); acid phosphatase/ protein serine/threonine phosphatase
263789.at	AT2G24550	241	2.00	0.00023	2.64	0.00002	2.64	0.000002	similar to unknown protein [Arabidopsis thaliana] (TAIRAT4G31510.1); similar to unknown [Populus trichocarpa x Populus deltoides] (GB:ABK96563.1)
263897.at	AT2G21940	241	2.83	0.00003	2.00	0.00003	2.46	0.000002	shikimate kinase, putative
266541.at	AT2G35110	241	3.03	0.00002	2.00	0.00002	2.30	0.000002	GR1_NAP1/NAPK (NACK-ASSOCIATED PROTEIN); transcription activator
248075.at	AT5G55730	235	2.46	0.00002	2.64	0.00002	2.00	0.000004	FLA1
248815.at	AT5G47050	235	2.83	0.00002	1.87	0.00002	2.80	0.000002	ATP binding / protein binding / shikimate kinase/ zinc ion binding
248896.at	AT5G45280	235	2.83	0.00002	1.87	0.00002	2.64	0.000552	pectinacetyltransferase, putative
249515.at	AT5G38530	235	2.46	0.00002	2.30	0.00002	2.30	0.000002	tryptophan synthase-related
250694.at	AT5G06710	235	1.87	0.000552	1.87	0.00006	3.73	0.000013	HAT14 (homeobox-leucine zipper protein 14); DNA binding / transcription factor
253512.at	AT4G31750	235	2.64	0.00006	2.00	0.00088	2.46	0.000008	protein phosphatase 2C, putative / PP2C, putative
253428.at	AT4G03340	235	2.64	0.00004	1.41	0.00007	3.48	0.000052	glyoxylate synthase family 14 protein / core 2/18-branched enzyme family protein
255428.at	AT4G20370	235	2.14	0.00001	2.14	0.00002	2.83	0.000023	AC9 (acetylcholine-dependent dioxygenase 1.1); oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-ox
255955.at	AT4G01700	235	2.30	0.00002	2.00	0.00002	2.83	0.000002	shikimate, putative
256756.at	AT3G25610	235	1.74	0.00006	1.87	0.00002	4.00	0.000002	haloacid dehalogenase-like hydrolase family protein
257028.at	AT3G19200	235	2.46	0.00002	1.62	0.000892	3.25	0.000004	similar to unknown protein [Arabidopsis thaliana] (TAIRAT4G34420.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN61148.1)
258857.at	AT3G02110	235	2.83	0.00052	2.14	0.000035	2.14	0.000046	SCPL25 (serine carboxypeptidase-like 25); serine carboxypeptidase
261397.at	AT1G79820	235	2.64	0.00002	1.74	0.00002	2.83	0.000048	SGBI-1; carbohydrate transmembrane transporter/sugar/hydrogen ion symporter
261405.at	AT1G27460	235	2.46	0.00002	2.14	0.00002	2.64	0.000002	OBP2 (OBP BINDING PROTEIN 2); DNA binding / transcription factor
262416.at	AT1G49390	235	2.00	0.00002	3.03	0.00002	2.14	0.000389	oxidoreductase, 2OG-Fe(II) oxygenase family protein
264501.at	AT1G09390	235	2.14	0.00002	2.64	0.000035	2.30	0.000002	GDSL-motif lipase/hydrolase family protein
268229.at	AT2G28840	235	2.46	0.00002	2.30	0.00002	2.30	0.000002	ankyrin repeat family protein
245060.at	AT2G39770	230	2.14	0.00002	1.87	0.00002	3.03	0.000002	CYT1 (CYTOKINESIS DEFECTIVE 1); nucleotidyltransferase
247480.at									



245141.at	AT2G45400	219	2.46	0.000035	2.00	0.000035	2.14	0.000167	BEN1: oxidoreductase, acting on CH-OH group of donors
248200.at	AT5G54160	219	2.64	0.00002	1.87	0.00004	2.14	0.00002	ATOMT1 (O-METHYLTRANSFERASE 1)
248019.at	AT5G44700	219	2.46	0.000023	2.30	0.00048	1.87	0.00049	ED23 (embryo sac development arrest 23): ATP binding / protein serine/threonine kinase
248011.at	AT5G23760	219	1.87	0.000027	2.64	0.00002	2.14	0.000046	heavy metal-associated domain-containing protein
250525.at	AT5G06550	219	2.64	0.00002	2.00	0.00006	2.00	0.00002	ILP1 (INCREASED LEVEL OF POLYPLD1Y-1D): translation repressor
251197.at	AT3G62960	219	2.00	0.00002	1.82	0.00013	3.25	0.00002	glutaredoxin family protein
251293.at	AT3G61930	219	2.46	0.00003	2.00	0.00023	2.14	0.00003	unknown protein
252943.at	AT4G39330	219	2.30	0.000046	1.74	0.00002	2.64	0.00004	mannitol dehydrogenase, putative
253317.at	AT4G39960	219	2.00	0.000774	2.64	0.00002	2.00	0.000088	similar to unknown protein [Arabidopsis thaliana] (TAIRAT2G15830.1)
254665.at	AT1G18250	219	1.83	0.000011	1.82	0.00014	5.26	0.00002	receptor serine/threonine kinase, putative
259713.at	AT1G17460	219	2.00	0.00013	2.00	0.00004	2.64	0.00002	binding
259823.at	AT1G66250	219	2.46	0.000023	2.00	0.00052	2.14	0.000052	glycosyl hydrolase family 17 protein
259956.at	AT1G17510	219	4.00	0.000046	2.00	0.00046	1.32	0.000052	RRA2 (REDUCED RESIDUAL ARABINOSE 2)
262452.at	AT1G11210	219	1.74	0.000966	2.83	0.00017	2.14	0.000101	similar to unknown protein [Arabidopsis thaliana] (TAIRAT1G11220.1); similar to cotton fiber expressed protein I [Gossypium hirsutum] (GBAAC332)
262677.at	AT1G15860	219	2.00	0.00002	2.00	0.00002	2.64	0.00002	similar to unknown protein [Arabidopsis thaliana] (TAIRAT1G20100.1)
267337.at	AT2G39200	219	2.14	0.000078	1.87	0.000023	2.64	0.00002	transferrin-binding protein
250233.at	AT5G13460	219	2.64	0.00002	2.00	0.00002	1.74	0.00003	IQG11 (IQ-domain 11): calmodulin binding
251937.at	KG5M040.AT3G53	219	2.64	0.00002	1.82	0.00003	2.46	0.00002	CGP049 (Conserved peptide upstream open reading frame 47) [Arabidopsis thaliana] (TAIRAT5G03190.1); similar to hypot
247333.at	AT5G63600	214	2.14	0.00002	2.14	0.00002	2.14	0.00002	flavonol synthase, putative
247377.at	AT5G63180	214	2.46	0.00002	1.87	0.00002	2.14	0.000052	pectate lyase family protein
247489.at	AT5G61830	214	2.14	0.00002	1.74	0.00002	2.64	0.00002	short-chain dehydrogenase/reductase (SDR) family protein
245556.at	AT5G50330	214	2.46	0.000069	2.14	0.000189	1.87	0.000055	ATP binding / protein kinase
246963.at	AT5G25750	214	2.30	0.00013	2.14	0.00002	2.00	0.00004	AHK2 (ARABIDOPSIS HESTIONE KINASE 2)
246784.at	AT5G24280	214	2.46	0.000241	2.30	0.000346	1.74	0.001077	ATP binding
246817.at	AT5G23820	214	2.30	0.00002	2.64	0.00002	1.62	0.000692	MD-2-related lipid recognition domain-containing protein / ML domain-containing protein
250149.at	AT5G14700	214	2.83	0.00002	1.52	0.000101	2.30	0.000023	cinnamoyl-CoA reductase-related
252319.at	AT4G34990	214	2.46	0.00002	1.82	0.000189	2.64	0.000023	AMYB32 (myb domain protein 32): DNA binding / transcription factor
254167.at	AT4G24400	214	2.46	0.00002	1.74	0.00002	2.30	0.00002	CPB8 (CBL-INTERACTING PROTEIN KINASE 8): kinase
254324.at	AT4G22460	214	1.87	0.00004	2.30	0.000027	2.30	0.000052	similar to unknown protein [Arabidopsis thaliana] (TAIRAT4G22466.1); similar to unknown protein [Arabidopsis thaliana] (TAIRAT4G22466.2); contains similar to unknown protein [Arabidopsis thaliana] (TAIRAT1G01360.1); similar to hypothetical protein [Vitis vinifera] (GBFAP63139.1); contains
255602.at	AT4G01026	214	2.30	0.00002	1.87	0.00002	2.30	0.00002	AZF2 (ARABIDOPSIS ZINC-FINGER PROTEIN 2): nucleic acid binding / transcription factor / zinc ion binding
257022.at	AT3G19580	214	1.62	0.005409	1.74	0.000214	3.48	0.00002	MYB30 (myb domain protein 30): DNA binding / transcription factor
257140.at	AT3G28910	214	1.87	0.00006	1.87	0.00002	2.83	0.00002	similar to unknown protein [Arabidopsis thaliana] (TAIRAT1G23710.1); similar to hypothetical protein [Vitis vinifera] (GBCAN1665.1); similar to unna
257226.at	AT3G27880	214	2.14	0.00002	1.87	0.00002	2.46	0.00002	similar to unknown protein [Arabidopsis thaliana] (TAIRAT1G23710.1); similar to hypothetical protein [Vitis vinifera] (GBCAN1665.1); similar to unna
257559.at	AT3G24120	214	2.30	0.00002	1.74	0.00002	2.46	0.00002	myb family transcription factor
257673.at	AT2G23990	214	2.14	0.00002	2.14	0.00002	2.14	0.00002	ID29 (IQ-domain 29): calmodulin binding
257868.at	AT3G25070	214	2.14	0.00002	1.87	0.00002	2.46	0.00002	RM4 (RPM1 INTERACTING PROTEIN 4): protein binding
259611.at	AT1G52280	214	2.00	0.00002	2.46	0.00002	2.46	0.00002	ARAB34 (Arabidopsis Rab GTPase homolog G34): GTP binding
260407.at	AT1G69910	214	3.03	0.000114	1.87	0.000114	1.74	0.004925	protein kinase family protein
260414.at	AT1G69850	214	2.46	0.00002	1.74	0.00002	2.30	0.00002	ATNR1.2 (NITRATE TRANSPORTER 1.2): calcium ion binding / transporter
260771.at	AT1G49690	214	2.46	0.000023	2.00	0.000023	2.30	0.00002	JAZ2 (JAZ1-LIKE JASMONATE-ZIM-DOMAIN PROTEIN 2)
260551.at	AT1G20590	214	2.14	0.00002	1.74	0.00002	2.64	0.00002	ICS: ribosomal protein S19 (RPS19)
260302.at	AT2G27050	214	2.30	0.00002	2.00	0.00002	2.14	0.00002	ELL (ETHYLENE-INSENSITIVE3-LIKE 1): transcription factor
260683.at	AT2G39400	214	1.52	0.000189	1.82	0.000346	4.00	0.00002	hydrolase, alpha/beta fold family protein
267069.at	AT2G41010	214	2.14	0.000966	2.00	0.000041	2.30	0.000068	ATCAMP25 (ARABIDOPSIS THALIANA CALMODULIN (CAM)-BINDING PROTEIN OF 25 KDa): calmodulin binding
245330.at	AT4G14930	209	2.30	0.00003	1.62	0.00002	2.46	0.00002	acid phosphatase survival protein SurE, putative
246494.at	AT5G16190	209	2.14	0.000101	2.00	0.000023	2.14	0.00013	ATCSLA11 (Cellulose synthase-like A11): transferase, transferring glycosyl groups
245538.at	AT5G11520	209	2.14	0.00002	2.00	0.00002	2.14	0.00002	glucanase family protein
246968.at	AT5G61720	209	2.30	0.000023	2.14	0.00002	1.87	0.00002	RLK (RECEPTOR-LIKE KINASE), ATP binding / kinase / protein serine/threonine kinase
247624.at	AT5G60160	209	2.14	0.00002	1.74	0.00002	2.46	0.000035	aspartyl aminopeptidase, putative
247734.at	AT5G59400	209	1.87	0.000273	1.82	0.000114	3.03	0.00002	similar to hypothetical protein [Vitis vinifera] (GBCAN4889.1)
248148.at	AT5G54930	209	2.00	0.000438	2.30	0.00002	2.00	0.000307	AT hook motif-containing protein
248154.at	AT5G54400	209	2.64	0.000114	1.74	0.001486	2.00	0.00002	methyltransferase
246962.at	AT5G49330	209	2.64	0.00002	2.00	0.00002	2.64	0.00002	regulator of divaricose condensation (RCC1) family protein
246777.at	AT5G24210	209	1.74	0.00002	1.52	0.00002	3.46	0.00002	lipase class 3 family protein
250735.at	AT5G06280	209	2.46	0.000966	1.74	0.000027	2.14	0.000035	similar to hypothetical protein [Vitis vinifera] (GBCAN7410.1)
253225.at	AT4G35020	209	2.00	0.00002	2.00	0.00002	2.30	0.00002	ARAC3/ATROP6/RHO1PS/ROP6 (rho-related protein from plants 6): GTP binding / GTPase
253603.at	AT4G30935	209	2.30	0.000241	1.87	0.00002	3.03	0.000023	WRKY32 (WRKY DNA-binding protein 32): transcription factor
253789.at	AT4G28400	209	2.14	0.000078	2.14	0.00002	2.30	0.00002	protein phosphatase 2C, putative / PP2C, putative
254363.at	AT4G22010	209	2.14	0.000101	2.30	0.00002	1.87	0.00002	SK54 (SKUS Similar 4): copper ion binding / oxidoreductase
254372.at	AT4G21620	209	2.14	0.00002	2.00	0.00002	2.14	0.00002	glycine-rich protein
254434.at	AT4G20880	209	1.74	0.000088	2.00	0.000035	2.64	0.00002	ethylene-responsive nuclear protein / ethylene-regulated nuclear protein (ERT2)
254520.at	AT4G19960	209	2.30	0.000068	1.87	0.00006	2.14	0.000088	potassium ion transmembrane transporter
255851.at	AT4G00940	209	2.46	0.00004	2.00	0.000307	1.87	0.000114	Dot-type zinc finger domain-containing protein
255990.at	AT4G03060	209	1.87	0.00003	1.62	0.00002	3.03	0.00002	CYP86A2 (ABERRANT INDUCTION OF TYPE THREE GENES 1): oxygen binding
256160.at	AT1G30120	209	2.30	0.00002	2.00	0.00002	2.14	0.00002	PEN1 (PENETRANT HYDROLYTIC DEHYDRONASE E1 BETA): pyruvate dehydrogenase (acetyl-transferring)
257121.at	AT3G26590	209	1.87	0.00003	2.14	0.00002	2.30	0.00002	MATE efflux family protein
258702.at	AT3G09730	209	2.64	0.000147	1.74	0.000438	2.00	0.00249	similar to unnamed protein product [Vitis vinifera] (GB-CAO18124.1)
259568.at	AT1G20490	209	2.14	0.000147	1.74	0.004073	2.46	0.000273	AMP-dependent synthetase and lipase family protein
259670.at	AT1G52310	209	2.46	0.00002	1.87	0.00002	2.00	0.00002	protein kinase family protein / C-type lectin domain-containing protein
259736.at	AT1G64390	209	2.83	0.00002	1.41	0.000023	2.30	0.00002	ATY9G2 (ARABIDOPSIS THALIANA GLYCOSYL HYDROLASE 9C2): hydrolase, hydrolyzing O-glycosyl compounds
261317.at	AT1G69790	209	2.14	0.000046	1.74	0.00002	2.46	0.000027	lipase class 3 family protein
261466.at	AT1G28440	209	2.30	0.00002	1.87	0.00002	2.14	0.000023	HS1 (HSEAS-LIKE 1): ATP binding / kinase / protein serine/threonine kinase
261552.at	AT1G63430	209	2.64	0.00002	1.87	0.00002	1.87	0.000685	leucine-rich repeat transmembrane protein kinase, putative
262882.at	AT1G75900	209	2.64	0.00002	2.14	0.000046	1.62	0.000389	family II extracellular lipase 3 (EXL3)
262736.at	AT1G28570	209	2.46	0.00002	2.00	0.000214	1.87	0.000068	GDSL-motif lipase, putative
263470.at	AT2G31900	209	2.00	0.000147	2.00	0.000074	2.30	0.000438	XIF (Myosin-like protein XIF)
263807.at	AT2G04400	209	1.87	0.000078	1.52	0.00002	3.25	0.00002	indole-3-glycerol phosphate synthase (IGPS)
264897.at	AT1G23220	209	2.00	0.00002	2.14	0.00002	2.83	0.00002	hypoxanthine-responsive family protein
265120.at	AT1G62640	209	2.14	0.00002	2.46	0.00002	1.74	0.00002	KAS III (3-HETOYLACYL CARRIER PROTEIN SYNTHASE III): 3-oxoacyl-[acyl-carrier-protein] synthase
266964.at	AT2G39480	209	2.00	0.00002	1.87	0.00002	2.46	0.00002	PGP6 (ATPase, coupled to transmembrane movement of substances)
267230.at	AT2G44080	209	1.87	0.002753	1.52	0.000035	3.73	0.000002	ARL (ARGOS-LIKE)
245853.at	AT5G13500	205	1.87	0.00002	2.30	0.00002	2.00	0.000147	similar to unknown protein [Arabidopsis thaliana] (TAIRAT5G25265.1); similar to unnamed protein product [Vitis vinifera] (GB-CAO42819.1)
246143.at	AT5G19980	205	2.14	0.00002	2.00	0.00004	2.00	0.00002	integral membrane family protein
245744.at	AT5G21760	205	2.00	0.00002	1.52	0.00002	2.83	0.00002	hypoxanthine-responsive family protein
248752.at	AT5G47600	205	4.00	0.00002	1.15	0.001201	1.87	0.001338	heat shock protein-related
248763.at	AT5G47550	205	2.46	0.000046	1.23	0.000374	2.83	0.00002	cysteine protease inhibitor, putative / cystatin, putative
249068.at	AT5G43980	205	2.30	0.00004	1.23	0.000355	3.03	0.00002	receptor-like protein kinase-related
249284.at	AT5G41810	205	2.14	0.00002	1.74	0.00002	2.30	0.00002	similar to unknown protein [Arabidopsis thaliana] (TAIRAT1G64340.1); similar to Avr9/Cf-9 rapidly elicited protein 194 [Nicotiana tabacum] (GBAAG)
249988.at	AT5G18310	205	2.14	0.00002	1.62	0.00002	2.46	0.00002	similar to unknown protein [Arabidopsis thaliana] (TAIRAT5G48500.1); similar to unnamed protein product [Vitis vinifera] (GB-CAO38794.1)
250515.at	AT5G09570	205	1.62	0.001077	2.46	0.000101	2.14	0.000041	similar to unknown protein [Arabidopsis thaliana] (TAIRAT5G64400.1); similar to unknown [Populus trichocarpa] (GBAB

**Supplemental Table S2.** Trichome and Trichome Branch Numbers of Transgenic Plants Harboring *GL2* Promoter-driven bHLH-GFP Genes.

	WT	<i>GL2pro-RHD6-GFP</i>	<i>GL2pro-LRL1-GFP</i>	<i>GL2pro-LRL1-GFP</i> × <i>GL2pro-RHD6-GFP</i>
Trichome number	243±51	224±33	230±53	131±39
1 branch (%)	0.5	0.9	0.9	0.7
2 branches (%)	3.7	5.0	4.7	7.4
3 branches (%)	94.5	91.4	92.2	81.7
4 branches (%)	1.3	2.7	2.2	9.9
5 branches (%)	0	0	0	0.3

The 10th–12th leaves of the wild type, homozygous transgenic lines (*GL2pro-RHD6-GFP* and *GL2pro-LRL1-GFP*), and the F1 progeny of the transgenic line (*GL2pro-RHD6-GFP* × *GL2pro-LRL1-GFP*) with a moderate trichome phenotype were observed. Numbers of trichomes on a leaf (mean ± s.d.,  $n = 20$ ) and ratios (%) of trichomes with each number of branches ( $n > 1,000$ ) are presented.

**Supplemental Table S3.** List of Primers Used in This Study.

Primer name	Sequence	Annotation
TUB2-real-F	GTTCTCGATGTTGTTTCGTAAG	for qRT-PCR
TUB2-real-R	TGTAAGGCTCAACCACAGTAT	
PLD $\zeta$ 1-real-F	CTTCTCTTGTGTGCCCAATG	
PLD $\zeta$ 1-real-R	CTGGTGCTATTCCCAAATCG	
LRL1-real-F	GTGCTGCTTCCGTTTCTTCT	
LRL1-real-R	GAGACAAAGACCTTTCCTTGA	
LRL2-real-F	CTGCTTCTGCTTCTTCTCAAATCTCTG	
LRL2-real-R	GTGGAGATGGTGGTGGCTAACGAG	
LRL3-real-F	TGTTGGACGAGATCATCGAG	
LRL3-real-R	TCCTGTAGCGTTTCCATTCC	
bHLH7-real-F	GCTGTCGCACCACTAGTCACTGAAA	
bHLH7-real-R	CTGGTGGCTGAGAATGGTAAATCGC	
bHLH59-real-F	GGTGCGGTTGCTCCACTTGTACTG	
bHLH59-real-R	TTTGATTGAAGAAGCTGCATCGCGG	
RHD6-real-F	TGATTTGGTGACAATGCTTGA	
RHD6-real-R	GGAGAGAATGGCATCAATGG	
RSL1-real-F	TGAGAAAGCAATTGGCTATGTAAAG	
RSL1-real-R	CTCGTTGTGATGATGAGAGGATTGC	
RSL2-real-F	AAAACAAGAGCCAGTCGTGGTGCAG	
RSL2-real-R	AAGCAATCGGCGCATAATCCATAG	
RSL4-real-F	GAAGAGAGAAGATTAACGAAAGGC	
RSL4-real-R	CAGGCCGTTGTAAGCCAATGGTGC	
bHLH84-real-F	GTTGATATTAGCACGATGTTGGAAG	

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bHLH84-real-R	TCTGGTCAGTGCATTGAGTTTTAGG	
ACT7-ChIP-F	CAGTCACGAGAAAAAAACCACAGTC	for ChIP
ACT7-ChIP-R	GGACATCGTTCAAATTTTATTCTCG	
PLDz1-ChIP-F	CTACATAGTATAAGATCACTGATTTG	
PLDz1-ChIP-R	CGACTTTGACCTCTCTCTCC	
LRL1-ChIP-F1	CAACAACAAAACAAATCATTAAACTACATGAAAAC	
LRL1-ChIP-R1	GTGCTAAGTGTAATAGCTAGCTTTTG	
LRL1-ChIP-F2	GTTTCATGTTAGCAATTAATGGAAAAGAGG	
LRL1-ChIP-R2	GTCCGGATGTTTGACACTTCTTC	
LRL1-ChIP-NF	TCATTGGGTAACACTTAGGTGGTCC	
LRL1-ChIP-NR	AAGGAGAATGATGAAACCAAACGAC	
LRL2-ChIP-F1	GCTTTCATGTTTCTCAAGTAGAG	
LRL2-ChIP-R1	GTCTTGGTTCTTACTCTATTAGTC	
bHLH82-ChIP-NF	CAAAAACAATTATACAAAGAGGCCG	
bHLH82-ChIP-NR	TACTGGCCGTTTCATTTGTTCTTTC	
RHD6-ChIP-F1	ATTTATTTACAATAATGTTGGGCG	
RHD6-ChIP-R1	TGCTTTCAAATAAAACATTCACACC	
RSL1-ChIP-F1	TTGATCTCATGCCAGCTTCCTCTC	
RSL1-ChIP-R1	TATCATAAAGGTTTATATAGGCGG	
RSL1-ChIP-F2	TAGATTGAATGTCATGCAACTTGGG	
RSL1-ChIP-R2	AAATACCACATTTACTTGGTCGTTC	
RSL2-ChIP-F1	TATCTAATGGTATCCCAGACTTG	
RSL2-ChIP-R1	ATAGTGGATAAATAAATGTCAAC	
RSL2-ChIP-F2	TGTTCTTAGTTTCGTAAATTAGATGG	

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RSL2-ChIP-R2	TCCCATCTATTTTGTGATTTGAAG	
RSL2-ChIP-F3	CGTCACATGACGTAAATCATAGTAAG	
RSL2-ChIP-R3	CACTATCTATCTCAGTTAAATGTGTATGAC	
eGFP-F	ATGGTGAGCAAGGGCGAGGAGC	for cloning*
eGFP-R	CTTGTACAGCTCGTCCATGCCG	
GL2-pF	AAGCTTTTGAATTGTAGATAAATCA	
GL2-pR	ACAAATCCTGTCCCTAGCTAGCTTCTTTGCTTAAT	
RHD6-pF	TTTTTCAAATGAGTTTTTATTTCTAGATT	
RHD6-pR	TAGACACTAATAAGTTTGATAAGTGATTTT	
RSL1-pF	ACCAATTGGTTAATCTTATAAGTCGCAC	
RSL1-pR	TGGTACTAAAGGGTGTCTAGTGAGATG	
RSL2-pF	CCTTTCTTTCCTATTTTTGTTCGTTT	
RSL2-pR	TTTTATATGTTTTGTTAACTAAGCGTC	
LRL1-pF	TCAATGAACTTATCCATGGTACG	
LRL1-pR	GATGATGATGGGTTTCTTCTGCTTC	
LRL2-pF	GAGGCGGTTGGGTTTAACGACCCG	
LRL2-pR	GGCTTCTGTTTTTTTTTTTTTTGGTGGGG	
GL2-CDSF	ATGTCAATGGCCGTCGACATGTCTT	
GL2-CDSR	TCAGCAATCTTCGATTTGTAGACTTCTCTT	
RHD6-CDSF	ATGGCACTCGTTAATGACCATCCC	
RHD6-CDSR	TTAATTGGTGATCAGATTCGAATTCC	
RSL1-CDSF	ATGTCACATTAACGAACATTGCAATG	
RSL1-CDSR	TTATTCTGCTATACTTGTCTCTAGTTG	
RSL2-CDSF	ATGGAAGCCATGGGAGAATGGAGC	

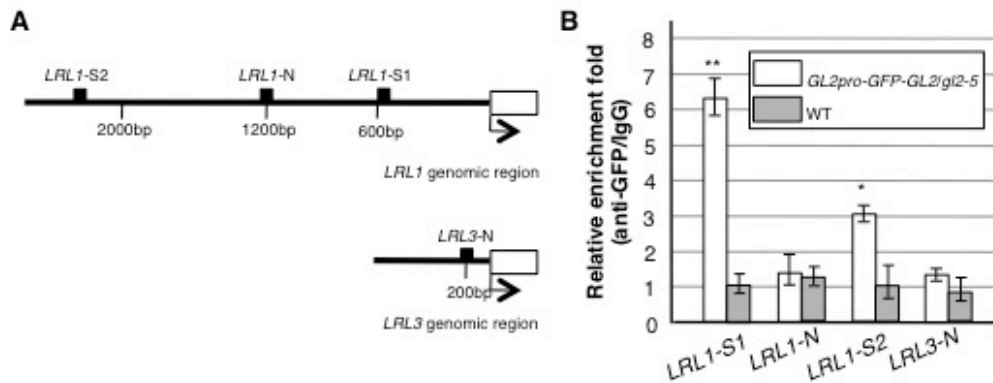
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RSL2-CDSR	TCATCTCGGTGAGCTGAGACCAATG	
LRL1-CDSF	ATGATGAACTCTTCTCTTCTAACTCCTTC	
LRL1-CDSR	TCACGCTTTCGAAACGGATACGGCCTC	
LRL1-genomicR	AGTGAAAAACCAATATACTATTTTTTTC	
LRL2-CDSF	ATGAACTCCTCGTCTCTTCTAACTCC	
LRL2-CDSR	TCACGGCTTGAAACGGAGGGAGCG	
gl2-5LB	GGATTTCCTGGGCAGAAGAGTA	for genotyping
gl2-5RB	GGATAGGGAGTGCGTCCAAGAG	
LBb1.3	ATTTTGCCGATTTTCGGAAC	
LRL1-1-LB	AGAAGACGACCTCTCGGTCAC	
LRL1-1-RB	GGGGTAATTCTTTTACAGAG	
LRL2-1-LB	GGACAAATGGCCGTTATCACGGCTTG	
LRL2-1-RB	GGACCACAAATTGCTACTAGTTTAGTAGG	
lrl1-2-TDNA-F	CAGCTACTGGTGGTACGGTGG	for checking of
lrl1-2-TDNA-R	GTCGACTGTATGGTCATGCCAG	T-DNA
lrl2-2-TDNA-F	CTCTCCCTTCCACCTCCCTC	insertion
lrl2-2-TDNA-R	GTTAGGAGACAAAGGAACGCCGG	

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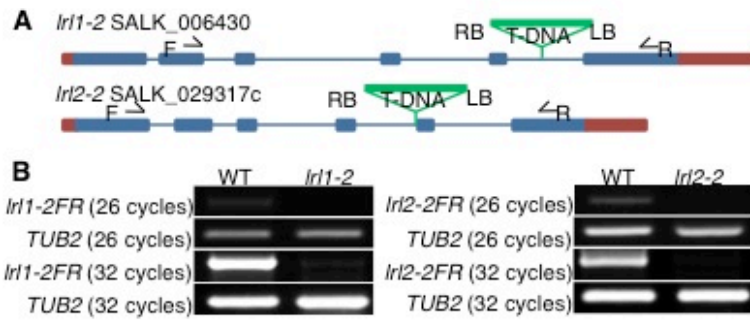
\*The recombination sites of the Gateway system were not included in these primers. Sequences of the recombination sites (see the Invitrogen Gateway™ Technology Instruction Manual) should be added when they are used in the Gateway system.



**Supplemental Figure S1.** ChIP Analysis for the GL2 Binding to the *LRL1* and *LRL3* Upstream Regions.

**(A)** The regions amplified in the ChIP analysis, *LRL1-S1*, *LRL1-N*, *LRL1-S2* and *LRL3-N*, are schematically illustrated. The L1 box-like sequence exists in *LRL1-S1* and *LRL1-S2*, but not in *LRL1-N* or *LRL3-N*.

**(B)** Results of the ChIP analysis of the regions illustrated in **(A)** are shown. Relative enrichment folds (anti-GFP/IgG) in *GL2pro-GFP-GL2/gl2-5* roots and wild-type roots are shown in white and gray boxes, respectively (mean  $\pm$  s.d.,  $n = 3$ ). Asterisks indicate that the enrichment in *GL2pro-GFP-GL2/gl2-5* is significantly different from that in the wild type (\*  $P < 0.05$ ; \*\*  $P < 0.01$ , Student's *t*-test).

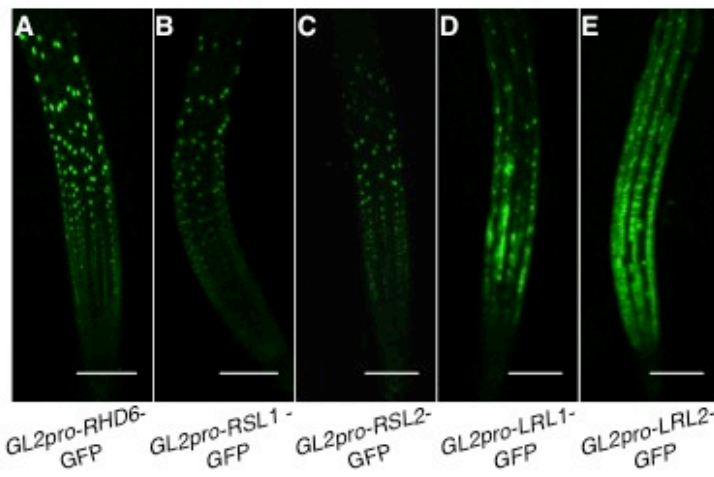


**Supplemental Figure S2.** Expression Analysis of the *lrl1-2* and *lrl2-2* Mutant Genes.

**(A)** The gene structures and T-DNA insertion sites of *lrl1-2* (SALK\_006430) and *lrl2-2* (SALK\_029317c) are schematically illustrated. Horizontal arrows labeled with F and R indicate the locations of the PCR primers used in **(B)**.

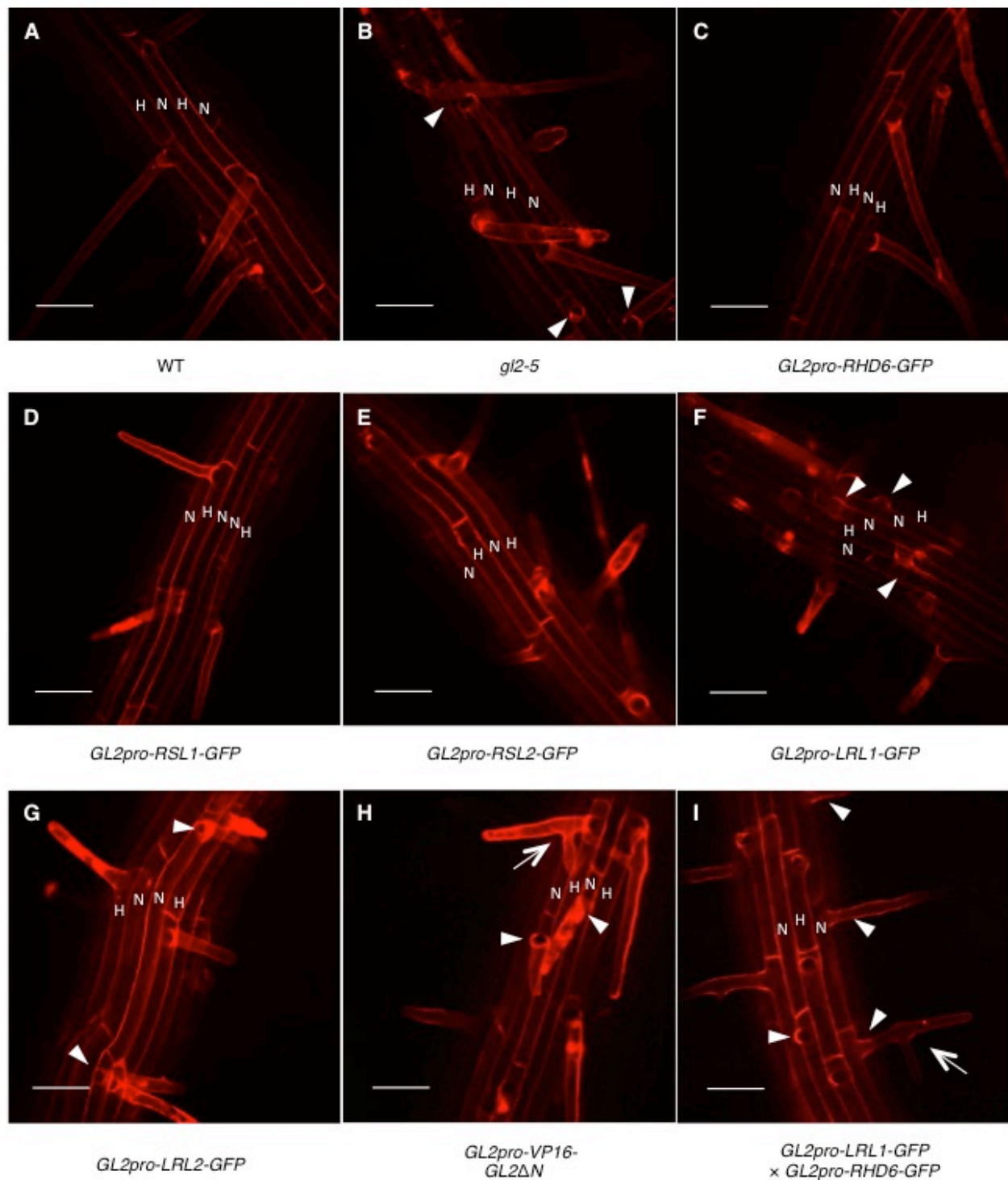
**(B)** The results of semi-quantitative RT-PCR analysis for *LRL1* and *LRL2* transcripts in wild-type and mutant plants are shown. Transcripts of the *TUBULIN2* (*TUB2*) gene were used as reference.





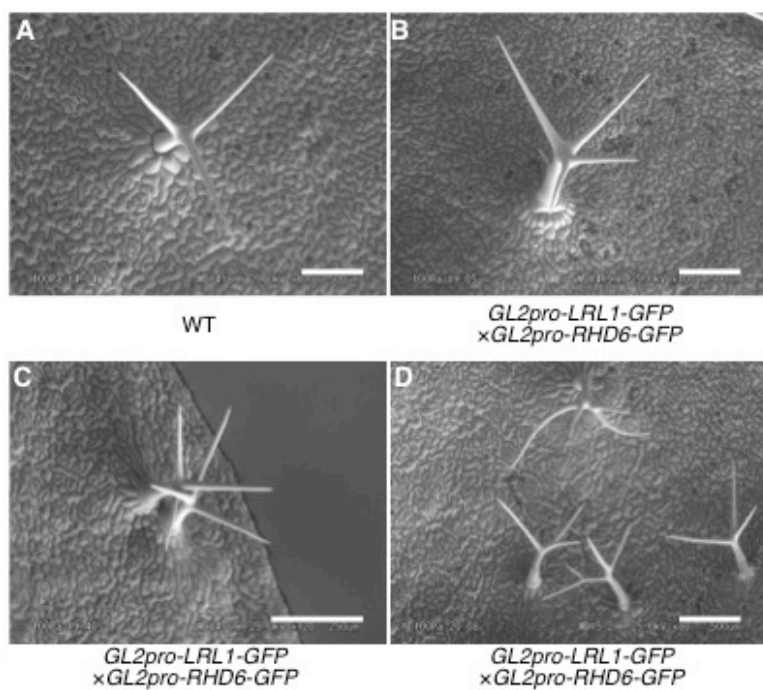
**Supplemental Figure S3.** Expression Patterns and Intensities of bHLH-GFP Fusion Proteins Driven by the *GL2* Promoter.

The GFP fluorescence signals in transgenic roots harboring *GL2pro-RHD6-GFP* (A), *GL2pro-RSL1-GFP* (B), *GL2pro-RSL2-GFP* (C), *GL2pro-LRL1-GFP* (D), and *GL2pro-LRL2-GFP* (E) are shown. Bar = 100  $\mu$ m



**Supplemental Figure S4.** Root Hair Development Patterns of the Transgenic Plants Harboring the *GL2* Promoter-driven bHLH-GFP Genes.

PI-stained Epidermal cells of wild-type (A) and *gl2-5* (B) roots, and transgenic roots harboring *GL2pro-RHD6-GFP* (C), *GL2pro-RSL1-GFP* (D), *GL2pro-RSL2-GFP* (E), *GL2pro-LRL1-GFP* (F), *GL2pro-LRL2-GFP* (G), *GL2pro-VP16-GL2ΔN* (H), and *GL2pro-LRL1-GFP* and *GL2pro-RHD6-GFP* (I) are shown. H and N cell files are marked by "H" and "N", respectively. Ectopic root hairs developing from N cell files and branching root hairs are indicated by arrowheads and arrows, respectively. Bar = 25 μm



**Supplemental Figure S5.** Trichome Phenotypes of Transgenic Plants Harboring Both *GL2pro-LRL1-GFP* and *GL2pro-RHD6-GFP*. Trichomes of wild-type plants (**A**) and transgenic plants harboring both *GL2pro-LRL1-GFP* and *GL2pro-RHD6-GFP* (**B to D**) are shown. Bar = 250  $\mu$ m

Site name	L1 box-like sequence
<i>PLD<math>\zeta</math></i> -S	5' -ATAGTATAAGATCACTGATTTGATTAATAAAATGTTAAGAAAATAA-3'
<i>CESA5</i> -S	5' -ACAGAAGAACAATAAGAGGGAAATAATAAAATGTTAAAGGGTGATC-3'
<i>MYB23</i> -S	5' -ATTATAAACATCTTGTGAAAAAGAATTTAAATGTACCCATTTTGTG-3'
<i>PAP2</i> -S	5' -AAATAATTAATAATTAATCAGATGATAAAATGTAATCAAATAAT-3'
<i>MYB113</i> -S	5' -ATGCACATAATTACTTAACCTAAGAACTAAATGTTGCATTGATTC-3'
<i>RHD6</i> -S	5' -TTACTCGCTCGGCCCATCAAAAATGAGTAAATGTTAACTGGTTTG-3'
<i>RSL1-S1</i>	5' -TATAACAAACAAAAATAAACTACATCTAAATGTCATCATTTAAT-3'
<i>RSL1-S2</i>	5' -CAAAACAAGTACCACGAACGACCAAGTAAATGTGGTATTTTTTT-3'
<i>RSL2-S1</i>	5' -TAGAGAACATGAGAGATAGTGGATAAATAAAATGTCAACACATAAT-3'
<i>RSL2-S2</i>	5' -AGTTTCGTAAATTAGATGGTTAATTTTTAAATGTTTCATCAAAAA-3'
<i>LRL1-S2</i>	5' -GACTACAAAATACAGACCTCGAAACCTTAAATGTATTAGTTAATG-3'
<i>LRL2-S</i>	5' -CAAATAAATAAACATATCTTATTTCCTTAAATGTAATTCATTCT-3'
Frequently appearing base	5' -AAA-AA <sup>A</sup> AAAAA--A-A-A-T-AA--A-TAAATGT-A-----T <sup>A</sup> <sub>T</sub> --3'

**Supplemental Figure S6. Sequences Surrounding the L1 Box-like Sites Recognized by GL2.**

DNA sequences surrounding the L1 box-like sites that have confirmed to be bound to GL2 individually by ChIP analysis are aligned. The sites *CESA5*-S, *MYB23*-S, *PAP2*-S, and *MYB113*-S correspond to the L1 box-like sites 802-, 2,372-, 1755-, and 837-base upstream from their initiation codons, respectively. The other sites are the same as those shown in Table II. The sites, *RSL2-S3-1*, *RSL2-S3-2*, *LRL1-S1-1*, *LRL1-S1-2*, and those in the *TT8* promoter region are omitted because they were examined for GL2 binding to more than one copy of the L1 box like-sequence. The L1 box-like sequence is highlighted. Frequently appearing bases (at 50% or higher) at each position are shadowed. The sequence composed of the frequently appearing bases is shown below the alignment.